

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers; and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: Jan

Searcher Phone #: 4498

Searcher Location: _____

Date Searcher Picked Up: 12/2/02

Date Completed: 12/2/02

Searcher Prep & Review Time: _____

Clerical Prep Time: 10

Online Time: 10

Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic ☒

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis _____

Sequence Systems ☒

WWW/Internet _____

Other (specify) _____

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 16.7172 Seconds
(without alignments)
1742.436 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613

Sequence: 1 MADQCGIEGVEDSAND.....EKKQIPCVSMULTKELYESQ 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	751	46.6	277	2	S64710
2	718	44.5	277	2	A55315
3	699	43.3	277	2	UC5410
4	580.5	36.0	212	2	167437
5	377	23.4	503	2	A49429
6	371.5	23.0	454	2	JC7123
7	354.5	22.0	416	2	G02635
8	349.5	21.7	495	2	T20038
9	317	19.7	435	2	A54821
10	305	18.9	452	2	JC6507
11	284	17.6	536	2	T43633
12	255	15.8	242	2	JC7517
13	250	15.5	642	2	T27021
14	246.5	15.3	488	2	T13851
15	210	13.0	418	2	B57511
16	199.5	12.4	182	2	167436
17	195	12.1	404	2	A42677
18	189.5	11.7	311	2	B56084
19	189.5	11.7	383	2	A56084
20	189.5	11.7	312	2	B54821
21	189	11.7	402	2	A46495
22	189	11.7	377	2	A57511
23	184	11.4	263	2	C56084
24	156.5	9.7	263	2	C56084
25	145.5	9.0	149	2	T43637
26	143.5	8.9	139	2	T43642
27	139	8.6	136	2	I53300
28	117	7.3	394	2	T26968
29	99.5	6.2	282	2	I84621

30	94.5	5.9	603	2	B64444	hypothetical prote
31	94.5	5.9	761	2	B97163	ATP-dependent seri
32	93.5	5.8	612	2	E84809	hypothetical prote
33	93	5.8	1151	2	T04657	hypothetical prote
34	93	5.8	1643	2	T07961	myosin heavy chain
35	91	5.6	1100	1	DD81D1	Rd1 protein - yea
36	91	5.6	1553	2	T18502	hypothetical prote
37	89.5	5.5	459	2	J00419	coagulation factor
38	89.5	5.5	857	2	T25465	hypothetical prote
39	87.5	5.4	1314	2	T47331	hypothetical prote
40	87.5	5.4	1358	2	A29360	Sir4 protein - yea
41	86	5.3	222	2	T26944	hypothetical prote
42	86	5.3	1004	2	JC2221	major surface glyc
43	86	5.3	1157	2	H69163	DNA helicase relat
44	85.5	5.3	330	2	T17593	mRNA guanylyltrans
45	85.5	5.3	486	2	A11942	cysteiny1-tRNA syn

ALIGNMENTS

RESULT 1

S64710
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S64710; S72395
R:Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 dur
A:Reference number: S64710; M0ID:96183185; PMID:8605870
A:Accession: S64710
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-277 <MAN>
A:Cross-references: EMBL:U27463
R:Wang, X.
submitted to the EMBL Data Library, May 1995

A:Reference number: S72395
A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
A:Cross-references: EMBL:U27463; NID:91244443; PIDN:AAB01511.1; PID:91244444
C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match

Best local Similarity 46.6%; Score 751; DB 2; Length 277;
Best local Similarity 52.4%; Pred. No. 2.5e-57;
Matches 150; Conservative 46; Mismatches 74; Indels 16; Gaps 3;

QY	18	NEPSVAKPDRSSVPSLFSK--KNVTRSIKTRDRVPTOYNNFEKIGCIINN	75
DB	4	NETSVDSKSIKNEVKTIHSGSKMSDSGIYDS-----SKNDYPMGVCIIINN	52
QY	76	KNPDYVGMGVRGTDRDAELFKPFRSLGPDVIVYNDSCAKMQLDLKASEEDHTAA	135
DB	53	KNHKSGTGMPPRSCTDPAKLRFTMNLKYEVANKNDLREVELLMKNSKEDHSRS	112
QY	136	CFPACILSHGEENVYIKGDGVTPKIDLTAFNRGDRCTLLKPLFTIOACRGELDDAI	195
DB	113	SFVCVILSHGDEGVIFGTDPIDLKLTYSFRGDRCSLIGKPLFTIOACRGTELCGI	172
QY	196	QANSGPINTDANPRKIPPEADPLFAYSTVPQYISRSRSGSDFVOALCSILEHGKE	255
DB	173	ETDSGCEDDMTQ--KIPEADEFLAVSTAPGYISWRNRDGSWFTQSLCSMLKLYAH	275
QY	256	LEIMQILTRVNDVAVRHFEESODPHREKKQIPCVSMULTKELXF	301
DB	230	LEPMHILTRVNRKVAPEFESFIDSTPHAKQIPCIYSMLTKELXF	275

RESULT 2

A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C:Accession: A55315, S58899, I39005
R:Bernardes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A:Title: CPP32, a novel human apoptotic protein with homology to *Caenorhabditis elegans*
A:Reference number: A55315; MUID:95074098; PMID:7983002.
A:Accession: A55315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <FER>
A:Cross-references: GB:U03737; NID:9561665; PIDN:AA65015.1; PID:9561666
R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, J.
Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A:Reference number: S58899; MUID:95319529; PMID:7596430.
A:Accession: S58899
A:Molecule type: protein
A:Residues: 29-46;176-189, 'E',191-193 <NIC>
R:Twierd, M.; Qian, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poitier
Cell 81, 801-809, 1995
A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A:Reference number: A56524; MUID:95292347; PMID:7774019
A:Accession: I39005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-189, 'E',191-277 <RES>
A:Cross-references: EMBL:U06943; NID:9857568; PIDN:AAA74929.1; PID:9857569
C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

[illegible]

C;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

[illegible]

RESULT 4
167437
cysteine proteinase (EC 3.4.22.-) p32 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67437
R:Flaws: J.A.; Kugu, K.; Tirdovich, A.M.; Desanti, A.; Tilly, K.I.; Hershfield, A.N...
E:Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian
nucosa cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67437
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RES>
A:Cross-references: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
C:keywords: cysteine proteinase; hydrolase

[illegible]

Cell 75, 641-652, 1993
A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
A:Reference number: A49429; MUID:94061982; PMID:8242740
A:Accession: A49429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-503 <YUA>
A:Cross-references: GB:I29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233
A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:P139826)
A:Accession: T37312
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417/R, 419-503 <YU2>
A:Cross-references: EMBL:L29052; PIDN:AAA27982.1
C:Genetics:
A:Gene: ced-3
A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 23.4%; Score 377; DB 2; Length 503;
Best Local Similarity 31.9%; Pred. No. 1,1e-24;
Matches 106; Conservative 49; Mismatches 117; Indels 60; Gaps 14;

6 GCIEOGVEDSANEDSVADKPRSSFVSLFSKKKN-VTKRSIKTKTDVPTVYNNF 64
187 GC-SLIGYSSSRNKSFSKA-----SGPTQYIFHEEDMNFVDAPTISRVDEKTMF--NF 238
65 EK-LGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAMODL 123
239 SSPGMCIIINNEHEQ---MPTNGTKADKNDLNLNFRMGVYVYICNDNLGRMLTI 295
124 KK-ASEEDTNAACFACILSLSHGEBNVIYKDGVT---PIKDLTAHFGDCKTLEKP 178
296 RDKFKHSHGDSAIL--VILSHGEEVNIIGVDPISTHEIYDLNANAPR--LANKP 350
179 KLEFIOACRGTELDIAQADSGPINDT-DANPRY----- 211
351 KIIVVQACRGRRNGF----PVLDSYGVPAFLRRGMNDNRGDFLNFEGCVRPOYQV 405
212 --KIPVADFLFAYSTVPGYVSRSPGRGSMFVQALCSILEHGKELIMQILTRVNDV 269
406 WRKRPQADILIAATVATQVYSNRNSARGSMFIOAVCEVFSHAKMDVVELTEVNKV 465
270 ARHESQSDDPHFHEKKQIPCVSMLEKLYF 301
466 ACGFOTSGS---NILKQMPMTSRLKKPFYF 494

RESULT 6
JC7123
C:Species: long chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9
A:Reference number: JC7123; MUID:20001956; PMID:10529400
A:Accession: JC7123
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <FUJ>
A:Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 23.0%; Score 371.5; DB 2; Length 454;
Best Local Similarity 32.8%; Pred. No. 3e-24;
Matches 90; Conservative 43; Mismatches 96; Indels 45; Gaps 6;

60 YNMNFKLGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAKM 119
191 YTLSDPGHCLITNNVFCSSGGLGTGSDNIDRDLKLEHFRMLRFMEVANKNDLTAKKM 250
120 QDLKKASEEDTNAACFACILSLSHGEE-----NVIYKDGVT-PIKDLTAHFGDRC 171

DB 251 VTALMAMAHNRHRAIDCFVYVILSHGQASHLQFPGAVYGTGCSYSIEKIYINFGSGC 310
OY 172 KTLLEKPKLFTIOACRGTELD-----AIOADSGPINDTDANPR----- 210
DB 311 PSLGKPKLFTIOACRGQKDHGFVACTSSQGRITLSDSDPDAPFPQGRPLDQDAV 370
OY 211 KPIVADFLFAYSTVPGYVSRSPGRGSMFVQALCSILEHGKELIMQILTRVNDV 270
DB 371 SSLPPSDILVSYTFPGVSWRDKKSGSWYETEDGILTFQWARSBDLQSLLRVANA 430
OY 271 RHESQSDDPHFHEK---KQIPCVSMLEKLYF 301
DB 431 -----EKGYTKQIPGCFNPLKKLFF 451

RESULT 7
G02635
ICE-LAP6 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02635
R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Polier, G.C.; Froelich, C.J.; He, W.W.; Dixi
submitted to the EMBL data library, April 1996
A:Reference number: H01513
A:Accession: G02635
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-416 <DUA>
A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AC50640.1; PID:g1336027

Query Match 22.0%; Score 354.5; DB 2; Length 416;
Best Local Similarity 32.1%; Pred. No. 7.9e-23;
Matches 88; Conservative 41; Mismatches 100; Indels 45; Gaps 6;

60 YNMNFKLGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAKM 119
153 YLSMEPCGHCLITNNVFCSSGGLGTGSDNIDRDLKLEHFRMLRFMEVANKNDLTAKKM 212
120 QDLKKASEEDTNAACFACILSLSHGEE-----NVIYKDGVT-PIKDLTAHFGDRC 171
213 VIALLELARQDHGALDCCVYVILSHGQASHLQFPGAVYGTGCGPVSVEKIYINFGTSC 272
172 KTLLEKPKLFTIOACRGTELDIAQADSGPINDTDANPRY----- 212
273 PSLGKPKLFTIOACRGEGQKDHGFVASTSPDESGSNPEPDAPFPQGLRTFDQDAI 332
OY 213 --IPVADFLFAYSTVPGYVSRSPGRGSMFVQALCSILEHGKELIMQILTRVNDV 270
DB 333 SSLPPSDILVSYTFPGVSWRDKKSGSWYETEDGILTFQWARSBDLQSLLRVANA 392
OY 271 RHESQSDDPHFHEK---KQIPCVSMLEKLYF 301
DB 393 -----VKGYTKQIPGCFNPLKKLFF 413

RESULT 8
T20038
hypochemical protein C48D1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20038
R:Burton, J.
submitted to the EMBL data library, October 1996
A:Reference number: Z19214
A:Accession: T20038
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-495 <WIL>
A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
A:Experimental source: clone C48D1
C:Genetics:
A:Gene: CESP:C48D1.2
A:Map position: 4

A:introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match

Best Local Similarity 21.7%; Score 349.5; DB 2; Length 495;

Matches 97; Conservative 48; Mismatches 87; Indels 81; Gaps 13;

22 VDAKPRSSFPVLPFSSKKKNVTMRISIKTRDRV-----PT-----YQYMMNF----- 64
 170 VNAFPQPSANSFT-----GCSLSGSSSRNNSFSKASPTQYIHEEDMNVDAPTIS 225
 65 -----EKL-----GKCIINNNKNDKVTGAGVRNGTDKDAEALFKCFRSLGFDVIYV 111
 226 RVFDEKTYRNFSPPRGMCILINNEHEQ---MPTNRGTADNDNLNLRGMYTICK 282
 112 NDCSCAKMODLKK-ASEEDHTNAACFACILSHGEBENVYKGDVT---PIKDLTAHF 166
 283 DMTGKMLTTRDFAKHSHGDSAIL--VILSHGEBENVIIIGVDIPISTHEIYDLNNA 340
 167 RGDRCETLEKPLFTFOACRGTELDADIAQDSGPINDT-DAMPY----- 211
 341 NMPR---LANKPRIVFOACRGERRNGF---PVLDSVGVPAFLRGRGMDNRDGPLFN 392
 212 -----KIPVEADFLFAYSTVPGYMSRSPGRSGFWOALCSILEHGEKELE 257
 393 FLGCVARPOVQVWRKKRPSQADILIAATATQIYVSMNSARGSFIOAVCEVSTHAKMD 452
 258 IMQILTRVNDRAV 270
 453 VVELLTENVKKVA 465

RESULT 9

A:54821

apoptosis regulator ICH-1, stimulatory form L - human
 C:Species: Homo sapiens (man)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C:Accession: A54821

R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.

Cell 78; 739-750; 1994

A:Title: Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative regulators

A:Reference number: A54821; MUID:94373811; PMID:8087842

A:Accession: A54821

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-435 <MAN>

A:Cross-references: GB:U13021; NID:9537291; PID:9537292

C:Keywords: alternative splicing; apoptosis

Query Match

Best Local Similarity 19.7%; Score 317; DB 2; Length 435;

Matches 75; Conservative 52; Mismatches 112; Indels 16; Gaps 6;

60 YMMNEKLGKCIINNNKNDKVTGAGVRNGTDKDAEALFKCFRSLGFDVIYVNDSCAKM 119
 175 YRLQSRPRGLALVLSVHTGKELEFRSGGDVDTLTFLKLLIDVHVLCDQTAQEM 234
 120 ODLLKASEEDHTNAACFACI--LSHGEENVYKGDG-VTPIKDLTAHFRGDRCKTLE 176
 235 QEKLNFAQLP-AHRYTDSICIVALLSHGVEGAIYGVGDKLLQGEVQLFDNANCSLON 293
 177 KKLEFFIOACRGTELDADIAQDSGP-----INDTDN---PRKIPEADELFAYST 225
 234 KRMFFIOACRGDEDRGVDODGKNHAGSPCEESDACKREKLPKMRLLPTRSDMIGYAC 353
 226 VPGYMSRSPGRSGFWOALCSILEHGEKELEIMQILTRVNDRAVHNFESQSDPRHNEK 285
 354 LKGTAAAMRTKGSWTIEALQVFSERACDMHVDMLAVN-ALIKDRGAYAPGTEFHNC 412
 286 KQIPCVSMLTRELY 300
 413 KEMSEYCSFLCRHLY 427

RESULT 10

JC6507

caspace-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: JC6507

R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.

Gene 202; 127-132; 1997

A:Title: Cloning and expression of the cDNA encoding rat caspace-2.

A:Reference number: JC6507; MUID:98087427; PMID:9427555

A:Accession: JC6507

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-452 <SAT>

A:Cross-references: GB:U7933; NID:92769705; PIDN:AAB96379.1; PID:92769706

Query Match

Best Local Similarity 18.9%; Score 305; DB 2; Length 452;

Matches 76; Conservative 55; Mismatches 110; Indels 18; Gaps 7;

58 YQ--YNNNFEKLGKCIINNNKNDKVTGAGVRNGTDKDAEALFKCFRSLGFDVIYVNDSC 115
 188 YQALVRLQSQPRGLALVMSVHTGKELEFRSGGDVDTLTFLKLLGYNVHLYDQT 247
 116 CAKMODLKKASEEDHTNAACFACI--LSHGEENVYKGDG-VTPIKDLTAHFRGDRCK 172
 248 AOEWQEKLNFAQLP-AHRYTDSICIVALLSHGVEGAIYGVGDKLLQGEVFLRPNANCP 306
 173 TLEKPLFTFOACRGTELDADIA-----QADSGPINDTDANP---RYKIPEADFLF 221
 307 SLQNKPRMFFIOACRGTEGRGVDDQDGKNHAGSPGCEESDAGEELMKMLPTRSDIC 366
 222 AYSTVPGYMSRSPGRSGFWOALCSILEHGEKELEIMQILTRVNDRAVHNFESQSDPH 281
 367 GYACIKNNAAMRTKRSWTIEALQVFSERACDMHVDMLAVN-ALIKDRGAYAPGTE 425
 282 FHEKKQIPCVSMLTRELY 300
 426 FHRCKEMSEYCSFLCRHLY 444

RESULT 11

T43638

caspace-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans

N:Contains: caspase 2B

C:Species: Caenorhabditis elegans

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T43638; T43639

R:Shaham, S.

J. Biol. Chem. 273; 35109-35117; 1998

A:Title: Identification of multiple Caenorhabditis elegans caspases and their potent

A:Reference number: 222587; MUID:99074291; PMID:9657046

A:Accession: T43638

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-826 <SHA>

A:Cross-references: EMBL:AF088288; NID:94063373; PIDN:AAC98295.1; PID:94063374

A:Accession: T43639

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 564-826 <SH2>

A:Cross-references: EMBL:AF088289; NID:94063375; PIDN:AAC98296.1; PID:94063376

A:Gene: csp-2

A:Map position: 4

C:Keywords: cysteine proteinase; hydrolase

Query Match

Best Local Similarity 18.9%; Score 305; DB 2; Length 826;

Matches 79; Conservative 53; Mismatches 96; Indels 36; Gaps 8;

57 TYOYNNFEKLGKCIINNNKNDKVTGAGVRNGTDKDAEALFKCFRSLGFDVIYVNDSC 116

```
Db 578 TRKRNRRSSKRAIINNVF---CGMEKRIGSDKDKKLSKLFERLQSTSYDNLKS 634
OY 117 AKMODLKKASEEDHTNAACFACILLSHGSENNVYIGDGYPIIDL-----TAHFQCD 169
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: J07517
R:Ecchard, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A:Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocy
A:Reference number: J07517; MUID:20517231; PMID:11062009
A:Contents: Epidermal keratinocytes
A:Accession: J07517
A:Molecule type: mRNA
A:Residues: 1-242 <ECC>
A:Cross-references: GB:AF097874
C:Comment: This enzyme accumulates during keratinocyte differentiation and is activat
C:Genetics:
A:Gene: casp-14/a
A:Map position: 19p13.1
A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C:Keywords: differentiation

Db 802 -DKVIVCKQAPFMSRRTKOLF 824

RESULT 12
T43633
caspase-related proteinase 1A (EC 3.4.22.-) - Caenorhabditis elegans
N:Contains: caspase 1B
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43633; T43636
R:Shaham, S.
J. Biol. Chem. 273, 35109-35117, 1998
A:Title: Identification of multiple Caenorhabditis elegans caspases and their potential
A:Reference number: 222587; MUID:99074291; PMID:9857046
A:Accession: T43633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-536 <SHA>
A:Cross-references: EMBL:AF088285; NID:94063367; PIDN:ACG98292.1; PID:94063368
A:Accession: T43636
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 269-536 <SH2>
A:Cross-references: EMBL:AF088286; NID:94063369; PIDN:ACG98293.1; PID:94063370
C:Genetics:
A:Gene: csp-1
A:Map position: 2
C:Function:
A:Description: probably acts in proteolytic cascades to regulate processes such as prog
C:Keywords: cysteine proteinase; hydrolase

Query Match 17.6%; Score 284; DB 2; Length 536;
Best Local Similarity 27.9%; Pred. No. 1,4e-16;
Matches 74; Conservative 50; Mismatches 109; Indels 32; Gaps 7;

OY 58 YQYNNMFEKLGKCIINNNKFDKVTGMGVNRTGDKDALELFKCRSLGFDVIVYNDSCA 117
Db 283 YCEMNSNPCTVILISNENF---KNMERVGTQKDEVNLTFLKQLOVTVICKRNLAE 339
OY 118 KMDDLKKAASEEDHTNAACFACILLSHGSENNVYIGDGYPIIDL-----TAHFQCD 172
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27021
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: 220299
A:Accession: T27021
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-642 <WIL>
A:Cross-references: EMBL:Z93393; PIDN:CA807698.1; GSPDB:GN00020; CESP:Y48E1B.13
A:Experimental source: clone Y48E1B
C:Genetics:
A:Gene: CESP:Y48E1B.13
A:Map position: 2
A:Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3; 487/1; 589/1; 609/3

Query Match 15.5%; Score 250; DB 2; Length 642;
Best Local Similarity 28.7%; Pred. No. 1.5e-13;
Matches 64; Conservative 41; Mismatches 94; Indels 24; Gaps 6;

OY 279 DPHFHEKKQIPCVVSMILTKELYSQ 303
Db 513 NVVL---KQAPFELSRLTKQMHFSR 534

RESULT 13
```

```
J07517
caspase-14/a - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: J07517
R:Ecchard, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A:Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocy
A:Reference number: J07517; MUID:20517231; PMID:11062009
A:Contents: Epidermal keratinocytes
A:Accession: J07517
A:Molecule type: mRNA
A:Residues: 1-242 <ECC>
A:Cross-references: GB:AF097874
C:Comment: This enzyme accumulates during keratinocyte differentiation and is activat
C:Genetics:
A:Gene: casp-14/a
A:Map position: 19p13.1
A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C:Keywords: differentiation

Query Match 15.8%; Score 255; DB 2; Length 242;
Best Local Similarity 28.0%; Pred. No. 1.6e-14;
Matches 69; Conservative 46; Mismatches 111; Indels 20; Gaps 5;

OY 59 QYNNMFEKLGKCIINNNKFDKVTGMGVNRTGDKDALELFKCRSLGFDVIVYNDSCA 118
Db 11 KYDMGATLALILCVTK-----AREGSEEDLDALEHMFQRLRFESTMKRDPTAQ 60
OY 119 MODLLK---ASEEDHTNAACFACILLSHGSENNVYIGDGYPIIDL-----TAHFQCD 174
Db 61 FOEELKFOQALIDREDPVSQAFVVLMAHGRGFLGEGEAVKLENEALNNKNCQAL 120
OY 175 LEKPLFTFOACRGTELDADAQADSGPINDTPANPRYPADELFVASTVPGYSSMS 234
Db 121 RAKKVVYITQACRGQRQRPGEVSGDELYMVKDSPTPTPTDALHYSTEGYIAHYH 180
OY 235 PGRGSMFVOALCSILEHKGLEIMQILTRVNDVRAHRESQSDPHFHEKKQIPCVSM 294
Db 181 DQKSGCFIOTLVDPYTK--RKGHILELLETVYRMAEALVQEG---KARKTNPETQST 234
OY 295 LTKELY 300
Db 235 LKRLY 240

RESULT 14
T27021
hypothetical protein Y48E1B.13 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27021
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: 220299
A:Accession: T27021
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-642 <WIL>
A:Cross-references: EMBL:Z93393; PIDN:CA807698.1; GSPDB:GN00020; CESP:Y48E1B.13
A:Experimental source: clone Y48E1B
C:Genetics:
A:Gene: CESP:Y48E1B.13
A:Map position: 2
A:Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3; 487/1; 589/1; 609/3

Query Match 15.5%; Score 250; DB 2; Length 642;
Best Local Similarity 28.7%; Pred. No. 1.5e-13;
Matches 64; Conservative 41; Mismatches 94; Indels 24; Gaps 6;

OY 58 YQYNNMFEKLGKCIINNNKFDKVTGMGVNRTGDKDALELFKCRSLGFDVIVYNDSCA 117
Db 361 YCEMNSNPCTVILISNENF---KNMERVGTQKDEVNLTFLKQLOVTVICKRNLAE 417
```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 10.4483 Seconds

(without alignments)
1202.814 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613

Sequence: 1 MADDOGCIIEEDGVEDSANED.....EKKQIPCVVSM/LTKELYSQ 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1606	99.6	303	1	ICE7_HUMAN
2	1394	86.4	303	1	ICE7_MESAU
3	1346	83.4	303	1	ICE7_MOUSE
4	744	46.1	277	1	ICE3_CRILLO
5	718	44.5	277	1	ICE3_HUMAN
6	716	44.4	277	1	ICE3_RAT
7	703	43.6	277	1	ICE3_MOUSE
8	662.5	41.1	299	1	ICE3_XENLA
9	552	34.2	282	1	ICE1_SPOFR
10	539	33.4	339	1	ICE1_DROME
11	532.5	33.0	323	1	ICE1_DROME
12	483.5	30.0	276	1	ICE6_MOUSE
13	466	28.9	293	1	ICE6_HUMAN
14	425.5	26.4	479	1	ICEA_HUMAN
15	395	24.5	521	1	ICEA_HUMAN
16	379	23.5	496	1	CEB3_CAEVU
17	377	23.4	503	1	CEB3_CAEVU
18	349.5	21.7	416	1	ICE9_HUMAN
19	343	21.3	424	1	ICE2_CHICK
20	317	19.7	435	1	ICE2_HUMAN
21	308	19.1	435	1	ICE2_MOUSE
22	255	15.8	252	1	ICEE_HUMAN
23	251.5	15.6	257	1	ICEE_MOUSE
24	234	14.5	382	1	ICEB_XENLA
25	228.5	14.2	386	1	ICEA_XENLA
26	219.5	13.6	410	1	ICEA_XENLA
27	211.5	13.1	377	1	ICEB_BOVIN
28	210	13.0	404	1	ICEB_CANPA
29	210	13.0	418	1	ICE5_HUMAN
30	203.5	12.6	312	1	ICE2_RAT
31	199.5	12.4	404	1	ICE2_RAT
32	198	12.3	405	1	ICE2_RAT
33	197	12.2	402	1	ICE2_RAT

34	195	12.1	404	1	11BC_HUMAN	P29466 homo sapien
35	190	11.8	373	1	ICEB_MOUSE	P70343 mus musculu
36	189	11.7	402	1	11BC_MOUSE	P29462 mus musculu
37	184	11.4	377	1	ICE4_HUMAN	P49662 homo sapien
38	177	11.0	419	1	ICEC_MOUSE	008736 mus musculu
39	171	10.6	480	1	CEFA_HUMAN	015519 h casp8 and
40	171	10.6	484	1	CEFA_MOUSE	035732 m casp8 and
41	99.5	6.2	282	1	FA9_RAT	P16296 rattus norv
42	94.5	5.9	603	1	YB55_MENJA	058555 methanococ
43	91	5.6	1100	1	RAD1_YEAST	P06777 saccharomyc
44	89.5	5.5	459	1	FA9_MOUSE	P16294 mus musculu
45	88.5	5.5	356	1	CARA_THETN	08rbk1 thermoaer

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	AA
ICE7_HUMAN	AC	P55210; 013364; Q96BA0;			
ICE7_HUMAN	DT	01-OCT-1996 (Rel. 34, Created)			
ICE7_HUMAN	DT	01-OCT-1996 (Rel. 34, last sequence update)			
ICE7_HUMAN	DT	15-JUN-2002 (Rel. 41, last annotation update)			
ICE7_HUMAN	DE	Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)			
ICE7_HUMAN	DE	(ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).			
ICE7_HUMAN	GN	CASP7 OR MCH3.			
ICE7_HUMAN	OS	Homo sapiens (Human).			
ICE7_HUMAN	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
ICE7_HUMAN	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
ICE7_HUMAN	OX	NCBI_TaxID=9606;			
ICE7_HUMAN	RP	SEQUENCE FROM N.A. (ALPHA ISOFORM).			
ICE7_HUMAN	RX	MEDLINE=96139498; PubMed=8576161;			
ICE7_HUMAN	RA	Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,			
ICE7_HUMAN	RA	Dixit V.M.;			
ICE7_HUMAN	RT	"ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans			
ICE7_HUMAN	RT	cell death protein Ced-3 is activated during Fas- and tumor necrosis			
ICE7_HUMAN	RT	factor-induced apoptosis."			
ICE7_HUMAN	RL	J. Biol. Chem. 271:1621-1625(1996).			
ICE7_HUMAN	RN	[1]			
ICE7_HUMAN	RP	SEQUENCE FROM N.A. (ALPHA ISOFORM).			
ICE7_HUMAN	RC	TISSUE=Spleen;			
ICE7_HUMAN	RX	MEDLINE=96147144; PubMed=8567622;			
ICE7_HUMAN	RA	Lippe J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;			
ICE7_HUMAN	RT	"Identification and characterization of CPP32/Mch2 homolog 1, a novel			
ICE7_HUMAN	RT	cysteine protease similar to CPP32."			
ICE7_HUMAN	RL	J. Biol. Chem. 271:1825-1828(1996).			
ICE7_HUMAN	RN	[3]			
ICE7_HUMAN	RP	SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).			
ICE7_HUMAN	RC	TISSUE=T-cell;			
ICE7_HUMAN	RX	MEDLINE=96105019; PubMed=8521391;			
ICE7_HUMAN	RA	Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,			
ICE7_HUMAN	RA	Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,			
ICE7_HUMAN	RA	Earnshaw W.C., Litwack G., Alnemri E.S.;			
ICE7_HUMAN	RT	"Mch3, a novel human apoptotic cysteine protease highly related to			
ICE7_HUMAN	RT	CPP32."			
ICE7_HUMAN	RL	Cancer Res. 55:6045-6052(1995).			
ICE7_HUMAN	RN	[4]			
ICE7_HUMAN	RP	SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).			
ICE7_HUMAN	RC	TISSUE=Petal lung, and Fetal spleen;			
ICE7_HUMAN	RX	MEDLINE=97224489; PubMed=9070923;			
ICE7_HUMAN	RA	Juan T.S.-C., McNeece I.K., Argente J.M., Jenkins N.A., Gilbert D.J.,			
ICE7_HUMAN	RA	Copeland N.G., Fletcher F.A.;			
ICE7_HUMAN	RT	"Identification and mapping of Casp7, a cysteine protease resembling			
ICE7_HUMAN	RT	CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."			
ICE7_HUMAN	RL	Genomics 40:86-93(1997).			
ICE7_HUMAN	RN	[5]			
ICE7_HUMAN	RP	SEQUENCE FROM N.A. (ALPHA ISOFORM).			
ICE7_HUMAN	RC	TISSUE=Skin;			
ICE7_HUMAN	RA	Strausberg R.;			
ICE7_HUMAN	RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.			
ICE7_HUMAN	RN	[6]			

RP PROCESSING.
 RA MEDLINE-65353838; PubMed-8755496;
 RA Fernandez-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trepiani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FAD0-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.
 CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ALPHA (SHOWN HERE), BETA AND
 CC ALPHA', ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS
 CC NOT PROTEOLYTICALLY ACTIVE.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,
 CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO
 CC EXPRESSION IN THE BRAIN.
 CC -1- PTM: CLEAVAGES BY GRAZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF. 4 AS BETA,
 CC BUT AS BETA IS ALREADY DEFINED IN REF. 3 WE HAVE CALLED IT ALPHA'.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U39613; AAC50346.1; -
 DR EMBL: U40281; AAC50352.1; -
 DR EMBL: U37448; AAC50303.1; -
 DR EMBL: U37449; AAC50304.1; -
 DR EMBL: U67319; AAC51152.1; -
 DR EMBL: U67320; AAC51153.1; -
 DR EMBL: U67206; AAC21460.1; -
 DR EMBL: BC015799; AAH15799.1; -
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.004; -
 DR GeneW: HGNC:1508; CASP7.
 DR MIM: 601761; -
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR PRINTS: PR00376; TLIBENZYM.E.
 DR SMART: SM00115; CASG. 1.
 DR PROSITE: PS01122; CASPASE_CYS. 1.
 DR PROSITE: PS01121; CASPASE_HIS. 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.
 FT PROPEP 1 23
 FT CHAIN 24 198
 FT PROPEP 199 206
 FT CHAIN 207 303
 FT ACT_SITE 144 144
 FT ACT_SITE 186 186
 FT VARSP_LIC 1 1
 FT VARSP_LIC 149 303

M -> MDCVMPGRKWHLEKNTSCGSSGICASYVTQM
 (IN ISOFORM ALPHA').
 VIYKDGVTPIKIDTAHFRGDRCKTLLEKPKLFIQACRG
 ELDDGICQADSGPINDTDANPRYKIPVEADLFAYSTVPGY

FT FT SWRSPGRSMFVQALCSILEHKGKDELMQILTRVNDRYAR
 FT HFEQSDDPHFHEKKQICPVVSMITKELFSQ -> MESCS
 FT VYQAGVORRDLGRLOPPRIALGSPSIMASAPTRGPMTO
 FT MLILTRSDQMKLTSSSPIDPRQATIRGAGQEPAPGCKRSA
 FT PSMRSTEXTWKACRSRSPG (IN ISOFORM BETA).
 FT C->A: NO APOPTOTIC ACTIVITY.
 FT CONFLICT 4 4 D -> E (IN REF. 5).
 FT CONFLICT 194 194 G -> A (IN REF. 1).
 SQ SEQUENCE 303 AA; 34276 MW; .CD373EE54A232CA4 CRC64;
 Query Match 99.6%; Score 1606; DB 1; Length 303;
 Best Local Similarity 99.3%; Pred. No. 1.5e-131;
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MADDDGCIIEOGVEVSANDSVDAKPDSSFPSPFSKKKKNTMTSITTRDRTYQY 60
 DB 1 MADDDGCIIEOGVEVSANDSVDAKPDSSFPSPFSKKKKNTMTSITTRDRTYQY 60
 QY 61 MNPFELGKCIILNNKNEPKVGMGRNCTDADAEALFCPSRLGPDVIVYNDSCAKMQ 120
 DB 61 MNPFELGKCIILNNKNEPKVGMGRNCTDADAEALFCPSRLGPDVIVYNDSCAKMQ 120
 QY 121 DLKRASEEDHTNAACFACILLSHGEENVYTKDGYTPIKDLTAHFRGDRCKTLLEKPK 180
 DB 121 DLKRASEEDHTNAACFACILLSHGEENVYTKDGYTPIKDLTAHFRGDRCKTLLEKPK 180
 QY 181 FFIQACRGTELDGIDQADSGPINDTDANPRYKIPVEADLFAYSTVPGYVSMSPGRGSM 240
 DB 181 FFIQACRGTELDGIDQADSGPINDTDANPRYKIPVEADLFAYSTVPGYVSMSPGRGSM 240
 QY 241 FVQALCSILEHKGKDELMQILTRVNDRYARFESQSDPHFHEKKQICPVVSMITKEL 300
 DB 241 FVQALCSILEHKGKDELMQILTRVNDRYARFESQSDPHFHEKKQICPVVSMITKEL 300
 QY 301 FSQ 303
 DB 301 FSQ 303
 RESULT 2
 ID ICE7_MESAU STANDARD: PRT; 303 AA.
 AC P55214;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 DE (SCA-2).
 GN CASP7 OR MCH3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Syrian; TISSUE=Liver;
 RX MEDLINE-96224303; PubMed-8643593;
 RA Pal J.-T., Brown M.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine
 RT protease that cleaves and activates sterol regulatory element binding
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

```

CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U47332; AAC52595.1; -
CC HSSP: P42574; 1PAU.
CC MEROPS: C14.004; -
CC InterPro: IPR002398; ICE.
CC InterPro: IPR002138; ICE_p10.
CC InterPro: IPR001309; ICE_p20.
CC Pfam: PF00655; ICE_p10; 1.
CC Pfam: PF00656; ICE_p20; 1.
CC PRINTS: PR00376; ILBCEZYME.
CC SMART: SM00115; CASC_1.
CC PROSITE: PS01122; CASPASE_CYS_1.
CC PROSITE: PS01121; CASPASE_HIS_1.
CC PROSITE: PS50207; CASPASE_P10; 1.
CC PROSITE: PS50208; CASPASE_P20; 1.
CC Hydrolase: Thiol protease; Zymogen; Apoptosis.
CC PROPEP 1 23
CC CHAIN 1 198 CASPASE-7 SUBUNIT P20.
CC PROPEP 199 206 BY SIMILARITY.
CC CHAIN 207 303 CASPASE-7 SUBUNIT P11.
CC ACT_SITE 144 144 BY SIMILARITY.
CC ACT_SITE 186 186 BY SIMILARITY.
CC SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 86.4%; Score 1394; DB 1; Length 303;
Best Local Similarity 84.2%; Pred. No. 3; 1e-113;
Matches 255; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 1 MADDCGIEEDGVEDSANDSVDAKPRSSFPVLSFKKKKNVYMSIKTRDRVPTQY 60
DB 1 MADDCNCAPELEKADPSGVDYDAKPRSSIISSILGKKKKNASACPVTARDRVPTLY 60
QY 61 MNMFELGKCIINNNKNDKYTGMYRNGTDDAEALFECFSLGADVYYINDSCAKMQ 120
DB 61 MNMFELGKCIINNNKNDKYTGMYRNGTDDAEALFECFSLGADVYYINDSCAKMQ 120
QY 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
DB 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
QY 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
DB 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
QY 181 FFIQACRGTELDLDAIQADSGPINDTANPRYKIPVEADLFAYSTVPGYYSNRPGRGSM 240
DB 181 FFIQACRGTELDLDAIQADSGPINDTANPRYKIPVEADLFAYSTVPGYYSNRPGRGSM 240
QY 241 FVQALCSITLHEHGRKLEIMQITLRVNDRAHAFESQSDPHHEKQICVYSMLTKELY 300
DB 241 FVQALCSITLHEHGRKLEIMQITLRVNDRAHAFESQSDPHHEKQICVYSMLTKELY 300
QY 301 FSO 303
DB 301 FGR 303

RESULT 3
ID ICE7_MOUSE STANDARD: PRT: 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.-C., McNiece I.R., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Workmanin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Graen M., Vandenaebale P., Declercq W., van den Brande I.,
RA van Looy G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U67321; AAC53068.1; ALT_INIT.
CC EMBL: D86353; BAA19730.1; -
CC EMBL: Y13088; CAA73530.1; -
CC EMBL: BC005428; AAH05428.1; -
CC HSSP: P42574; 1PAU.
CC MEROPS: C14.004; -
CC MGD: MGI:109383; Casp7.
CC InterPro: IPR002398; ICE.
CC InterPro: IPR002138; ICE_p10.
CC InterPro: IPR001309; ICE_p20.

```

DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILIBCEZYME.
 DR SMART: SM00115; CASC. 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR Hydrolyase: Thiol protease; Apoptosis.
 KW PROPEP 1 23
 FT CHAIN 198
 FT PROPEP 24
 FT CHAIN 199
 FT CHAIN 207
 FT ACT_SITE 144
 FT ACT_SITE 144
 FT ACT_SITE 186
 FT CONFLICT 10
 FT CONFLICT 45
 FT CONFLICT 48
 FT CONFLICT 49
 SO SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match 83.4%; Score 1346; DB 1; Length 303;
 Best Local Similarity 81.5%; Pred. No. 4.4e-109;
 Matches 247; Conservative 27; Mismatches 29; Indels 0; Gaps 0;

QY 1 MADDQCIIEGVEDSANEDSVDAKPDSSFPVLSFKKKKNTVMSIKTRPRVPTQY 60
 DB 1 MTDDQCAAELEKVDSSSEDEVDKPDSSIISSILKKRNASGPRVGTGDRPTLYL 60

QY 61 NMNEKLGKCLIIINNNKDFKVTGKVRNGTDKDAELFKCFRSLGFDVIVYNDSCAKM 120
 DB 61 RMDQKMGKCIINNNKDFKATGMVNRNGTDKDALFKCFRSLGFDVIVYNDSCAKM 120

QY 121 DLTKASEEDHSHSCFVLSHEEDLYGKGVTPIKDLTAHFDRDCKTLLKPKL 180
 DB 121 DLTKASEEDHSHSCFVLSHEEDLYGKGVTPIKDLTAHFDRDCKTLLKPKL 180

QY 181 FFIOACRGTDLDDGIQADSGPINIDANPRKIPVADFLAYSTVPVYMSRSPGRSGM 240
 DB 181 FFIOACRGTDLDDGIQADSGPINIDANPRKIPVADFLAYSTVPVYMSRSPGRSGM 240

QY 241 FVQALCSLIEHGKLELMQILTRVNDVARNHSESQDPHFHEKKQIPCVVSMLTKELY 300
 DB 241 FVQALCSLIEHGKLELMQILTRVNDVARNHSESQDPHFHEKKQIPCVVSMLTKELY 300

QY 301 FSR 303
 DB 301 FSR 303

RESULT 4
 ICE3_CRILLO STANDARD: PRT: 277 AA.

AC 060431;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Cricetus longicaudatus (Long-tailed hamster) (chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OC NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=66183185; PubMed=8605870;
 RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during apoptosis.";

RL EMBL J. 15:1012-1020(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROPEPASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U27463; AB01511.1;
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.003; -.
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR002138; ICE_p10.
 CC InterPro: IPR001309; ICE_p20.
 CC Pfam: PF00655; ICE_p10; 1.
 CC Pfam: PF00656; ICE_p20; 1.
 CC PRINTS: PR00376; ILIBCEZYME.
 CC SMART: SM00115; CASC. 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS50207; CASPASE_P10; 1.
 CC PROSITE: PS50208; CASPASE_P20; 1.
 CC KW Hydrolyase; Thiol protease; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 28
 FT CHAIN 29
 FT CHAIN 176
 FT ACT_SITE 121
 FT ACT_SITE 163
 SO SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2B28A3 CRC64;

Query Match 46.1%; Score 744; DB 1; Length 277;
 Best Local Similarity 52.1%; Pred. No. 4.1e-57;
 Matches 149; Conservative 46; Mismatches 75; Indels 16; Gaps 3;

QY 18 NEDSVDAKPDSSFPVLSFKKK--KNVTMSIKTRPRVPTQYNNMFEKLGKCIINN 75
 DB 4 NETSVDSIKNFKEVKTILGSKMSDGIYLD-----SYKMDPEGVGVCIIINN 52

QY 76 KNPKYVGMVNRNGTDKDAELFKCFRSLGFDVIVYNDSCAKMODLTKASEEDHTNAA 135
 DB 53 KNFKRSTGMPRSGVDVAALRETFMALKYEVNRKNDLTREIYELMKNASKEDHSKRS 112

QY 136 FCACILSHGGEENIYGDVTPIKDLTAHFGRDCKTLLKPKLFFIOACRGTDLDDGI 195
 DB 113 SFQVILSHGDEGVIFGDPIDLKLITSTYRGDYCRSLIGKPKLFFIOACRGTDLDDGI 172

QY 196 QADSGPINDDANPRKIPVADFLAYSTVPVYMSRSPGRSGMFWQALCSLIEHGKRE 255
 DB 173 ETDGTEEDMTQC--KIPVADFLAYSTAGYVSWNRKPDGSMFIQSLCSMLKLYAHK 229

QY 256 LEIQILTRVNDVARNHSESQDPHFHEKKQIPCVVSMLTKELY 301
 DB 230 LEFMHILTRVNRKVAETEFSFSLDSTFPAKKQIPCVVSMLTKELY 275

RESULT 5
ICE3_HUMAN STANDARD; PRT; 277 AA.
ID ICE3_HUMAN PRT; 277 AA.
AC P42574;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT Interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764(1994).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Belder D.R., Porter G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
[3]
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
RX MEDLINE=95319529; PubMed=7596430;
RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
RA Gallant N.A., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.T., Li V.L.;
RA Miller D.K.;
RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";
RL Nature 376:37-43(1995).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96263532; PubMed=8673606;
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant N., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apoptin/CPP32, a key mediator of
RT apoptosis.";
RL Nat. Struct. Biol. 3:619-625(1996).
[5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle J.P., Tomaselli K.J., Grutter M.G.;
RT Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Valda K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Demolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Haltiwanger R.C., Liang P.H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";

RL J. Biol. Chem. 275:16007-16014(2000).
[7]
RN PROCESSING.
RP MEDLINE=96353838; PubMed=8755496;
RX Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FAD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
[8]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apoptin, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
[9]
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
CC CLEAVAGE OF HUNTINGTIN.
CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE. AND LOW
CC IN TESTES. ALSO FOUND IN MANY CELL LINES. HIGHEST EXPRESSION IN
CC CELLS OF THE IMMUNE SYSTEM.
CC -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U13737; AAA65015.1; -;
DR EMBL: U13738; AAB60355.1; -;
DR EMBL: U26943; AA474929.1; -;
DR PDB: 1PAU; 07-JUL-97.
DR PDB: 1CP3; 24-DEC-97.
DR PDB: 1GFR; 23-JUN-00.
DR MEROPS: C14.003; -;
DR Genew: HGNC:1504; CASP3.
DR MIM: 600636; -;
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PRO0376; ILIHCENYME.
DR SMART: SM00115; CASC.1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KW 3D-structure. 1 9
FT PROPEP

FT PROPEP 10 28
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT VARIANT 190 190
 FT SEQUENCE 277 AA: 31594 MM; 8E34DD2ACE6E6F64B CRC64;
 SO
 Query Match 44.5%; Score 718; DB 1; Length 277;
 Best Local Similarity 50.5%; Pred. No. 7.3e-55;
 Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;
 QY 19 EDSVAKPDRSEFVSLSKKKNTMRSIKTRBDRVPTGYVNMNPKGKIIINNNKF 78
 DB 5 ENSVDSKSIK NLEPKIIGHSEMSMSGISLDNS-----TKMDPEKGLCIIINNNKF 55
 QY 79 DKVTGMVANGTGDAAELFKCFRSLGFDVIVYNDSCAKMODLLKKAEEEDHTNACPA 138
 DB 56 HKSTGMSRSGTDVDAANLRETFRNLKYEVRNKNLDTREIYELMRDYSKEDHSKRSSFV 115
 QY 139 CILSHGSEENVYKGDVTPPIKDLTAHRRGDRCKTLLEKPLFTIOACRGTFLDIDAIOAD 198
 DB 116 CVLLSHGEGIIIFGTNGFVDLKKITNFRGDRCSRSLTGKPKLFIIOACRGTFLDGIETD 175
 QY 199 SGPIINDTANPRYKIPVADFLFAYSTVPGYVSRSPGRSGMFGVALSILEHKELEI 258
 DB 176 SGVDDDMAC---HKIPVADFLFAYSTVPGYVSRNSDGSFIOSLCAMLKQYADKLEF 232
 QY 259 MOILTRVNDVRAHREESODDPHFHEKROICPVVSMLEKELF 301
 DB 233 MHILTRVNRKVAETEFSFSDATFPAKKQICVISMLEKELF 275

RESULT 6
 ID ICE3_RAT STANDARD; PRT: 277 AA.
 AC P55213; P70543; Q62993; P97699;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNeice I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desautel A., Tilly K.I.,
 RA Hirschfeld A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RT of the ovarian follicle.";
 RL Endocrinology 136:5042-5053(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=97184204; PubMed=9030616;

RA NI B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Hockey P.K.,
 RA Rostock P. Jr., Poirier G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-1beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569(1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RC Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
 CC ELEMENT BINDING PROTEIN (SREBP) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
 CC BUT NOT IN KIDNEY OR TESTIS.
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
 CC ADULT BRAIN.
 CC -1- PFM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U49930; AAC52765.1; -;
 DR EMBL: U34685; AAC52261.1; -;
 DR EMBL: U84410; AAB4192.1; -;
 DR EMBL: U58656; AAB02722.1; -;
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.003; -;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR PRINTS: PR00376; ILIBCEZYME.
 DR SMART: SM00115; CASC.1
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 29 28
 FT CHAIN 176 175
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT ACT_SITE 25 29
 FT CONFLICT 170 170
 FT CONFLICT 178 178
 FT CONFLICT 182 182
 FT CONFLICT 187 187
 FT CONFLICT 190 190
 FT CONFLICT 199 199
 FT CONFLICT 211 211
 D -> G (IN REF. 2).
 C -> S (IN REF. 2).
 T -> A (IN REF. 2).
 M -> V (IN REF. 2).
 I -> K (IN REF. 2).
 E -> G (IN REF. 3).
 T -> S (IN REF. 2).
 D -> G (IN REF. 2).

FT CONFLICT 236 236 L -> I (IN REF. 4).
 FT CONFLICT 245 245 T -> M (IN REF. 3).
 SQ SEQUENCE 277 AA, 31491 MW, ADABFA18E2507402 CRC64;
 Query Match
 Best Local Similarity 50.3%; Pred. No. 1,1e-54;
 Matches 144; Conservative 44; Mismatches 82; Indels 16; Gaps 3;
 DB 1: Length 277;
 18 NEDSVADKPRDSRSEVSLPSKKK--KNVTMRSLKTRDRVPTQYNNMFELGKCIINN 75
 4 NEDSVDSKSIINNETKTINGSKSMDSGIYDS-----SYKNDYEMGICIIINN 52
 76 KNEPKTGVGNKGTDKDAEALFKCRSLGFDVIYVNDSCAMQDLKKAASEDHNTAA 135
 53 KNEHKTGASRNGTVDVDAANLREFMALKEVYRNKNLDRREIMELMDSVSKEDHSKRS 112
 136 CFCACILSGEEVYVYKGVPTIKDLTAHFRRDRCKTLLKPKLPFTQCRGTDLDAI 135
 113 SFVCVILSHGDSGVITGTGKPVDLKLTSPFRGDYCRSLGKPKLFIQACRGTELDGI 172
 196 QADSGFINPTDANPRYKIPVEADFLFAYSTVPGYVSWRSPRGSMFVQALCSILEHGKE 255
 173 EDSGCTDDMACO--KIYEADFLAYSTAFYTSRNRSDGSWFLQSLCAMLKLYAKK 229
 256 LEIMQILTFVNDVARNHFEESQSDPHHEKKQIPCVVSMLTKELYF 301
 230 LEFMHILTRVNRKVATEFEFSFLDATHFAKKQIPCIYVSMLTKELYF 275
 RESULT 7
 ICE3_MOUSE STANDARD: PRT: 277 AA.
 ID ICE3_MOUSE
 AC P70677: 008668:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apolipin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1) (ICE).
 CN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T. S.-C., McNelece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
 RT activation of CPP32 in the apoptosis induced by a withdrawal of
 RT NGF.";
 RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/An;
 RA MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenberghe P., Declercq W., van den Brande I.,
 RA van Ioo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (May 1997) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROBABLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES SPEROL REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
 CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
 CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOSOL.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
 CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
 CC TESTIS.
 CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.slb.ch).
 CC -----
 CC EMBL: U54803; AAC52768.1; -;
 CC EMBL: U54802; AAC52768.1; JOINED.
 CC EMBL: U49929; AAC52764.1; -;
 CC EMBL: D86352; BAA21727.1; -;
 CC EMBL: Y13086; CA73528.1; -;
 CC EMBL: U19522; AAC53196.1; -;
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.003; -;
 CC MGD: MG1:107739; Casp3.
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR002138; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC Pfam: PF00655; ICE_P10; 1.
 CC Pfam: PF00656; ICE_P20; 1.
 CC SMART: SM00135; CASC.1
 CC PROSITE: PS01122; CASPASE_CTS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS50207; CASPASE_P10; 1.
 CC PROSITE: PS50208; CASPASE_P20; 1.
 CC KMW Hydrolyase; Thiol protease; zymogen; Apoptosis.
 CC PROPEP 1 9
 CC PROPEP 10 28
 CC CHAIN 29 175
 CC CHAIN 176 277
 CC ACT_SITE 121 121
 CC ACT_SITE 163 163
 CC CONFLICT 17 17
 CC CONFLICT 51 51
 CC CONFLICT 84 84
 CC CONFLICT 95 95
 CC CONFLICT 97 97
 CC CONFLICT 128 128
 CC CONFLICT 135 135
 CC CONFLICT 135 135
 SQ SEQUENCE 277 AA, 31474 MW, CE9159BF74826605 CRC64;
 Query Match
 Best Local Similarity 43.6%; Score 703; DB 1; Length 277;
 Matches 146; Conservative 40; Mismatches 83; Indels 18; Gaps 4;

or send an email to license@slb.ch.

EMBL: U81510; AAC47442.1; -

HSSP: P42574; ICP3.

DR MEROPS: C14.015; -

DR InterPro: IPR002138; ICE_P10.

DR InterPro: IPR001309; ICE_P20.

DR Pfam: PF00655; ICE_P10; 1.

DR Pfam: PF00656; ICE_P20; 1.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS01020; CASPASE_P10; 1.

DR PROSITE: PS01020; CASPASE_P20; 1.

DR Hydrolyase: Thiol protease; Zymogen; Apoptosis.

FT PROPEP 1 28

FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.

FT PROPEP 185 195 POTENTIAL.

FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.

FT ACT_SITE 136 136 BY SIMILARITY.

FT ACT_SITE 178 178 BY SIMILARITY.

FT FT

SEQUENCE 299 AA: 33527 MW: 99FAFED09B04EED6 CRC64:

Query Match 34.2%; Score 552; DB 1; Length 299;

Best Local Similarity 40.5%; Pred. No. 1,8e-40;

Matches 122; Conservative 52; Mismatches 109; Indels 18; Gaps 7;

12 GVEDSANEDSVDAKP-----DRSFPVPSLFSSKKKKVNRISIKTTDRVPTVOYNNFE 65

4 GKQDNGNVDSDIKQRTNGGDEGDLGSSSSOPNRVAMPV---DRNAPV-TNNMHK 58

66 KLGKCIINNNKNDKYTGMGVNGRTGDADALFKCFERSLGFDVIVYNDSCACAKMODLLK 125

59 HRGMALIFNHEHD-ILSLKSRGTGTVNDNLKLVKLTGFKVTFEFLNKSEELNKRIQ 117

126 ASEEDITNACFCILLSHEENVITGKGVTPKIDLTANFRGDRCKTLLEKPLFTIQ 185

118 TAMDHSDDCLLVAVLTGELMLYAKDPHYKPDNLMYFTADKCPPLGKPLFTIQ 177

186 CRCTEDDADIAQDSGPINDANP--RYKIPVEADFLFAYSTVPGYVSWSPGSGMFVQ 243

178 CGQDRLDGGLTISR---TETDGSPTSSTYRIPVHADFLIATSTVPGYVSMNRTTSGSMFQ 234

244 ALCSILEHGKLEIMQILRVNDRVARHSES--DDPHFEKKOIPCVYSMLTKELFYS 302

235 ALCEEELRYAGTERDILTLTLFVQKVALDEFSANAPDSAMHQQKQVCIITSMLTRLVFG 294

303 Q 303

295 K 295

RESULT 10

ICE_DROME STANDARD; PRT; 339 AA.

01-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Caspase precursor (EC 3.4.22.-) (drfice).

ICE OR CG7788.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

SEQUENCE FROM N.A.

TISSUE=embryo;

MEDLINE=97327558; PubMed=9184225;

Fraser A.G., Evan G.I.;

"Identification of a Drosophila melanogaster ICE/CED-3-related

RT protease, drfice.";

EMBO J. 16:2805-2813(1997).

[2]

SEQUENCE FROM N.A.

STRAIN=Berkeley;

MEDLINE=20196006; PubMed=10731137;

ADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltskov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,

Burtis K.C., Bussan D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,

Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

GADECK A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,

Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Rabinet K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA GIBBS R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

-1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOWNSTREAM OF RPR.

CC CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITRO.

CC -1- SUBUNIT: HETERODIMER OF A 21 kDa (P21) AND A 12 kDa (P12) SUBUNIT.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES WHERE APOPTOSIS

OCCURS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed, usage by and for commercial

CC entities requires a license agreement (See <http://www.slb.ch/announce/>

CC or send an email to license@slb.ch).

EMBL: Y12261; CAAT2937.1; -

EMBL: AE003771; AAF56939.1; -

DR HSSP: P42574; IPAU.

DR MEROPS: C14.015; -

DR FlyBase: FBgn0019972; ICE.

DR InterPro: IPR002396; ICE.

DR InterPro: IPR002138; ICE_P10.

DR InterPro: IPR001309; ICE_P20.

DR Pfam: PF00655; ICE_P10; 1.

DR Pfam: PF00656; ICE_P20; 1.

DR PRINTS: PR00376; ILICENZYME.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01122; CASPASE_CYS; 1.


```

FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215
FT CHAIN 216 323 CASPASE-1 SUBUNIT P13.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35926 MW; B5F0FF75EB8E2BD CRC64;

Query Match
Best Local Similarity 44.6%; Score 532.5; DB 1; Length 323;
Matches 111; Conservative 47; Mismatches 80; Indels 11; Gaps 6;

OY 59 OYVNMNEKIKGKCIINNNKNDKVTGMGVNRTGDKDAELKCRSLGFDYIVYNDSCAK 118
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
70 ETNMSKHGVALIFNHFEPD-IPSLKSRGTGVNDQELKAFENLGFVSVHDC---K 125
OY 119 MODLLK---KASEEDHTNACFACILSHGEENVYKGDVTPFKDITAFHRGRCKTL 175
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
126 LBDLKHVKAKAELDTNDCLAVALLSHGHEHYLAKDQYKLDNIWIKFTATFCPSLA 185
OY 176 EKPKLFFIACRGTELDDAIQADSGPINDTD--ANPKYKIPVADFLFAYSTVPGYYSWR 233
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
186 GKPKLFFIACRGDRIDGITLEKG-VTETDGESESTSYKIPHADFLFSYSTIPGVESWR 244
OY 234 SPGRSMFVQALCSILEHCKELEIMQILTRVNDVRAHRESO-SDDPHFEKKQIPCV 292
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
245 NINNGSMVWQSLIRELNAGKKYDLTLTLTFVNQVALDFESNVPAIPMDRQKQIPCLT 304
OY 293 SMLTKELYF 301
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
305 SMLTKELRF 313

RESULT 12
ICE6_MOUSE STANDARD: PRT: 276 AA.
AC 008738:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
van Looy G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
CC -I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -I- SUBUNIT: HETERODIMER OF A 18 KDA (P18) AND A 11 KDA (P11) SUBUNIT
(BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, KIDNEY,
TESTIS, AND HEART. LOWER LEVELS IN SPLEEN, SKELETAL MUSCLE, AND
BRAIN.
CC -I- PM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
SUBUNITS (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y13087; CAA73529.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS; C14.005; -.
DR MGD; MGI:1312921; Casp6.
DR Interpro: IPR002398; ICE.
DR Interpro: IPR002138; ICE_P10.
DR Interpro: IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT CHAIN 1 162
FT PROPEP 163 176
FT CHAIN 177 276
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 276 AA; 31595 MW; 5965DE932112686C CRC64;

Query Match
Best Local Similarity 30.8%; Score 483.5; DB 1; Length 276;
Matches 99; Conservative 43; Mismatches 104; Indels 9; Gaps 2;

OY 56 PTYOYNNPEKIKGKCIINNNKNDKVTGMGVNRTGDKDAELKCRSLGFDYIVYNDSC 115
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
16 PAEOYKMDHKRRGVALIFNHFEPD-IPSLKSRGTGVNDQELKAFENLGFVSVHDC---K 125
OY 116 CAMMODLLKRASEEDHTNACFACILSHGEENVYKGDVTPFKDITAFHRGRCKTL 175
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
76 AEELLKIHVSTSSSHIDACFCIFLSHGEGNIVAYADKIELQTLGLFGKGCOSLV 135
OY 176 EKPKLFFIACRGTELDDAI-----QADS-GPINDTDANPKYKIPVADFLFAYSTV 226
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
136 GKPKLFFIACRGSDHVPVPLDMVDHQTDLNDVTQVDAASYTLFAGADFLMCSVA 195
OY 227 PGYYSRSPGRSMFVQALCSILEHCKELEIMQILTRVNDVRAHRESO-SDDPHFEKK 286
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
196 EGYSHRETVNGSMYIQLCEMLARYGSSLEFTELLTVNKKYSORRVDFCKDPAIGKK 255
OY 287 QIPCVVSMLELYF 301
Db :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
256 QVPCFASMLTKLHF 270

RESULT 13
ICE6_HUMAN STANDARD: PRT: 293 AA.
AC P55212:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6 OR MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93516841; PubMed=7796396;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene
family.";
RL Cancer Res. 55:2737-2742(1995).

```

RN [2]
 RP PROCESSING.
 RC TISSUE-Lymphocytes;
 RX MEDLINE-97059171; Pubmed-8900201;
 RA Srinivasula S.M., Fernandes-Alnemri T., Zangirilli J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RT "The Ced-3/Interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-cleaving enzyme Mcn2alpha are substrates for the apoptotic
 RT mediator CPP32.";
 RL J. Biol. Chem. 271:27099-27106(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
 CC POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
 CC PROGRAMMED CELL DEATH.
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM DOES NOT
 CC SEEM TO HAVE PROTEOLYTIC ACTIVITY.
 CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
 CC SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U20536; AAC50168.1; -;
 DR HSSP: U20537; AAC50169.1; -;
 DR HSSP: P42574; 1PAU.
 DR Genew; HGNC:1507; CASP6.
 DR MIM: 601532; -;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR PRINTS: PR00376; IL1BENZYM.
 DR SMART: SM00115; CASC.1
 DR PROSITE: PS01122; CASPASE_CYS.1.
 DR PROSITE: PS01121; CASPASE_HIS.1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 FT PROPEP 1 23
 FT CHAIN 24 179 CASPASE-6 SUBUNIT P18.
 FT PROPEP 180 193
 FT CHAIN 194 293 CASPASE-6 SUBUNIT P11.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARSPLIC 14 102 MISSING (IN ISOFORM BETA).
 SQ SEQUENCE 293 AA; 33409 MW; BD9204E23CE1F670 CRC64;
 Query Match 28.9%; Score 466; DB 1; Length 293;
 Best Local Similarity 37.9%; Pred. No. 4,7e-33;
 Matches 97; Conservative 42; Mismatches 107; Indels 10; Gaps 1;

DB 153 GKPXIFITQACGNOHDVPIPLDWDVNOTEKIDNITEVDASVYTLGADFLMCYSV 212
 QY 226 VPGYSSMRSPGRGSMNVQALGSLIEHGEKLEIMOLTFEVNDVAVHFEQSDDPHHEK 285
 DB 213 AGCYTSRHTVGVSWITDQCEMLGKRGSSLEFTELLTVNKRVSORRVDFCKOPSAIGK 272
 QY 286 KOIPCVSMTRKELYP 301
 DB 273 KOVPCFASMLTKKLHF 288
 RESULT 14
 ICE8_HUMAN
 ID ICE8_HUMAN STANDARD; PRT; 479 AA.
 AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;
 AC Q15806; Q9U081; Q14676;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
 DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
 DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
 DE (Apoptotic protease Mch-5) (CAP4).
 GN CASP8 OR MCH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Thymus, and B-cell;
 RX MEDLINE-96279826; Pubmed-8681376;
 RA Boldin M.P., Goncharov T.M., Golitsev Y.V., Wallach D.;
 RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death.";
 RL Cell 85:803-815(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-96279827; Pubmed-8681377;
 RA Muzio M., Chinaiyalyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Krammer P.H., Peter M.E., Dixit V.M.;
 RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
 RL Cell 85:817-827(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE-96353838; Pubmed-8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99132295; Pubmed-9931493;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human Casp8 gene.";
 RL Gene 226:225-232(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
 RX MEDLINE-97373543; Pubmed-9228018;
 RA Srinivasula S.M., Ahmed M., Ottillie S., Bullrich F., Banks S.,
 RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armstrong R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis.";
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN [6]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE-97121412; Pubmed-8962078;

FT VARSPIC 274 521 MISSING (IN ISOPFORM C).
FT CONFLICT 68 68 E -> G (IN REF. 2).
FT CONFLICT 268 268 T -> A (IN REF. 3).
FT CONFLICT 410 410 V -> I (IN REF. 3).
SQ SEQUENCE 521 AA; 58950 MW; 840348AE602B243 CRC64;

Query Match 24.5%; Score 395; DB 1; Length 521;
Best Local Similarity 30.4%; Pred. No. 1.3e-26;

Matches 95; Conservative 55; Mismatches 99; Indels 64; Gaps 9;

QY 11 QGVEDSANEDSV---DAKPDRS-----SFVPSLFSKKKKKNTMRSI--KT 50
Db 209 QGEELVYSQTDVFTFLPALFOESMOKNHAGSNGNRATNGAPSLVSRGMOGASANTLNSET 268
QY 51 TDREVPPTYQYNMNEFKLGKCIINNKNFDKVTGMGVRNGTDDKAELFKCFRSLGFDVIV 110
Db 269 STKRAAVYRRNRRNR--GLCVIVNNHSF---TSLKDRGTHKDAELLSHYFQWLGFTYHI 323
QY 111 YNDCSCAKMODLKKAS--EEDHTNACFCACILLSHGEENVYKGD-GVTPIKDILTAFHFRG 168
Db 324 HNNVTKEMEMVLQOKKCNPAHADGDFVFCILTHGRFGAVYSSDEALIPIREITMSHTA 383
QY 169 DRCKTLEKPKLFIFQACRGTELDALQADSGPINDTA--NPRYKIPVEADFLFAISTV 226
Db 384 LQCPRLAEKPKLFIFQACQGEELIOPSVSIEADALNPEQAPTSLQDSIPAEDFLGLATV 443
QY 227 PGYYSNRSRPGSGMFOALGSLIEHGEKELEIMQILTRVNDRVARHFEESQDDPHFEKK 286
Db 444 PGYVSFRHVEGSMYIOSLCN-----HLKK 468
QY 287 QIPCVYSMLTKEL 299
Db 469 LVPRLMLKLEKTM 481

Search completed: December 2, 2002, 12:56:29
Job time : 11.4483 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 28.7328 Seconds
(without alignments)
2172.860 Million cell updates/sec

Title: us-09-895-263-2

Perfect score: 1613
Sequence: 1 MADQGCIEEGVDSANED.....EKKQPCVSMILKELYFSQ 303

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_TREMBL_21:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_mhc:*
9: SP_Organelle:*
10: SP_Phage:*
11: SP_Plant:*
12: SP_Rodent:*
13: SP_Virus:*
14: SP_Vertebrate:*
15: SP_Unclassified:*
16: SP_Xvirus:*
17: SP_bacteriap:*
18: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1395	86.5	303	11	088550	088550 ratu
2	1025	63.5	318	13	091B65	091B65 xenopus lae
3	744.5	46.2	282	13	098U18	098U18 brachydanio
4	743	46.1	283	13	093417	093417 gallus gall
5	721	44.7	277	4	096AN1	096AN1 homo sapien
6	720.5	44.7	277	6	095ND5	095ND5 sus scrofa
7	719	44.6	277	4	096KP2	096KP2 homo sapien
8	623.5	38.7	220	11	090W14	090W14 mus musculu
9	512.5	31.8	304	13	091B66	091B66 xenopus lae
10	510	31.6	303	13	091B66	091B66 xenopus lae
11	500.5	31.0	302	13	091B66	091B66 xenopus lae
12	493.5	30.6	182	6	077623	077623 oncorhynch
13	483.5	30.0	276	11	099M47	099M47 mus musculu
14	481	29.8	277	11	035397	035397 ratu
15	474	29.4	293	4	0980E7	0980E7 homo sapien
16	473.5	29.4	276	11	0980E9	0980E9 mus musculu

17	447.5	27.7	480	11	089110	089110 m caspase 8
18	446.5	27.7	482	13	090W01	090W01 gallus gall
19	446	27.7	308	5	09NHFP	09NHFP drosophila
20	446	27.7	308	5	09VET9	09VET9 drosophila
21	444.5	27.6	479	4	08WY08	08WY08 homo sapien
22	443	27.5	482	11	09JHX4	09JHX4 ratu
23	425.5	26.4	538	4	08RD15	08RD15 homo sapien
24	423.5	26.3	496	4	09COK4	09COK4 homo sapien
25	414.5	25.7	399	13	09IB63	09IB63 xenopus lae
26	411.5	25.5	326	5	09GV88	09GV88 hydra atten
27	396	24.6	476	13	091B63	091B63 brachydanio
28	377.5	23.4	454	11	091B63	091B63 mus musculu
29	372.5	23.1	403	13	090W02	090W02 gallus gall
30	371.5	23.0	520	13	091B62	091B62 xenopus lae
31	364.5	22.6	454	11	09JHX1	09JHX1 ratu
32	362	22.4	500	13	091B64	091B64 xenopus lae
33	356.5	22.1	416	4	09B062	09B062 homo sapien
34	317	19.7	435	4	09BUP7	09BUP7 homo sapien
35	314.5	19.5	417	5	09Y106	09Y106 pristionchu
36	309	19.2	423	13	091B67	091B67 xenopus lae
37	305	18.9	263	5	09TZP5	09TZP5 caenorhabdi
38	305	18.9	452	11	055194	055194 ratu
39	305	18.9	826	5	09Y055	09Y055 caenorhabdi
40	284	17.6	268	5	09TZP6	09TZP6 caenorhabdi
41	284	17.6	536	5	018203	018203 caenorhabdi
42	275.5	17.1	393	11	09R0S9	09R0S9 mus musculu
43	255.5	15.8	450	5	09XYF4	09XYF4 drosophila
44	255	15.8	347	5	09GV89	09GV89 hydra atten
45	252	15.6	339	4	08TD13	08TD13 homo sapien

ALIGNMENTS

RESULT 1
088550 PRELIMINARY: PRT: 303 AA.
ID 088550:
AC 088550:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Forghani F., Roy S.;
RT "Rat caspase-7 sequence."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF072124; AAC24011.1;
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.004; -.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; IIBCNZYME.
DR SMART: SM00115; CASP. 1.
DR PROSITE: PS01122; CASPASE_CYS. 1.
DR PROSITE: PS01121; CASPASE_HIS. 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; A71728754BF199DD CRC64;

Query Match 86.5%; Score 1395; DB 11; Length 303;
Best Local Similarity 84.5%; Pred. No. 1.3e-119;
Matches 256; Conservative 21; Mismatches 26; Indels 0; Gaps 0;
QY 1 MADQGCIEEGVDSANEDSVDAKPRSSFPVSLFSSKKKNVTRISIKTRDRRYPTQY 60

```
Db 1 MDDDOCAAELEADSSDEGVADAKDRSTISSLKMKKKNASMCVPSTTRRVPYLY 60
Oy 61 NMNFEKLCIIINNNKFKVTGMVNRNGTDKDAEALFKCFRSLGFVYIYNDCSCAKM 120
Db 61 RMDFEKMGCIINNNKFKATMDVNRNGTDKDAEALFKCFRSLGFVYIYNDCSCAKM 120
Oy 121 DLKKAASEBDHTNAACFACILLSHGSEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
Db 121 DLLRRASEBDHNSACFACILLSHGSEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
Oy 181 FFIQACRGTELDIAIDAGSPINDTDANPRYKIPVEADELFAYSTVPGYYSWSPGRGSW 240
Db 181 FFIQACRGTELDIAIDAGSPINDTDANPRYKIPVEADELFAYSTVPGYYSWSPGRGSW 240
Oy 241 FVOALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELX 300
Db 241 FVOALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELX 300
Oy 301 FSO 303
Db 301 FGR 303
```

RESULT 2

PRELIMINARY: PRT: 318 AA.

```
AC 091B65;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-7.
GN XCASPASE-7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038170; BAB94748.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR Pfam; PF00655; ICE_p10; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 318 AA; 35937 MW; 6EBC6684AF86A128 CRC64;
```

Query Match 63.5%; Score 1025; DB 13; Length 318;

Best Local Similarity 65.6%; Pred. No. 1,le-85;

Matches 196; Conservative 33; Mismatches 64; Indels 6; Gaps 2;

```
Oy 9 EEOGVEDSANDSVDAKDRSSFPVSLFSKKKNYTMRSIKT---TRDVPPTYOYNNMF 65
Db 17 DEPREEEGEDSVDAKDRSOFISSTKKKVEDKPKTNNNVRYTPAFQYKMMNG 76
Oy 66 KLGGKIIINNNKFKVTGMVNRNGTDKDAEALFKCFRSLGFVYIYNDCSCAKMODLKK 125
Db 77 NVGRCIINNNKFKITGMGARGNTDIDARELLRCFKGIGFDVYVYNNKSCSEMENTLRT 136
```

```
Oy 126 ASEBDHTNAACFACILLSHGSEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 185
Db 137 VAQODHDSACFACIFLSHGSEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 196
Oy 186 CRGTLEDIAIDAGSPIND---TDANPRYKIPVEADELFAYSTVPGYYSWSPGRGSWF 242
Db 197 CRGHEFDGLEDAGSGVNDSELTETDANPRYKIPVEADELFAYSTVPGYYSWSPGRGSWF 256
Oy 243 QALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELX 301
Db 257 QALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELX 315
```

RESULT 3

PRELIMINARY: PRT: 282 AA.

```
AC 098U18;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR 2FIN; ZDB-GENE-011210-1; casp3.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;
```

Query Match 46.2%; Score 744.5; DB 13; Length 282;

Best Local Similarity 47.6%; Pred. No. 4,6e-60;

Matches 147; Conservative 50; Mismatches 67; Indels 45; Gaps 5;

```
Oy 7 CIEQGVEDS-ANED-----SVDAKDRSSFPVSLFSKKKNYTMRSIKTTRDRVPT 57
Db 5 CYDAKRVDTTDSKDGASASOPWQVDAKPOSHA----- 38
Oy 58 YOYNNMFEKLCIIINNNKFKVTGMVNRNGTDKDAEALFKCFRSLGFVYIYNDCSCA 117
Db 39 -KSLNYPNIGACIIINNNKFKATMDVNRNGTDKDAEALFKCFRSLGFVYIYNDCSCA 97
Oy 118 KMDDLKKAASEBDHTNAACFACILLSHGSEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 177
Db 98 QIMQVLTVAHDHSCASLVCYLLSHGDEGVFEGTDSVDLSLSLRGDRCKTLLEKPKL 157
Oy 178 PLFFIQAACRGTELDIAIDAGSPINDTDANPRYKIPVEADELFAYSTVPGYYSW 233
Db 158 PLFFIQAACRGTELDIAIDAGSPINDTDANPRYKIPVEADELFAYSTVPGYYSW 212
Oy 234 SPGRSMFVQALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVS 293
Db 213 NTMTGSWFIQALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVS 272
```

QY 294 MLTKELYFS 302
Db 273 MLTKELYFT 281

RESULT 4

093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgman J.T.;
RT "Caspase-3 and -6 expression, and enzyme activity in hen granulosa
cells".
RL Biol. Reprod. 62:589-598(2000).
EMBL: AF083029; AAC32602.1; -;
DR HSP; P42574; 1PAU.
DR MEROPS: C14.003; -;
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; IL1BCENZME.
DR SMART: SM00115; CASC.1
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFDACF CRC64;

Query Match 46.1%; Score 743; DB 13; Length 283;
Best Local Similarity 52.4%; Pred. No. 6.4e-60;
Matches 150; Conservative 44; Mismatches 76; Indels 16; Gaps 5;

QY 17 ANDSDYAKDRSSFPVLSKSKKNVTMRISIKTRDRV-PTYQNNMFEKLGKCIINN 75
Db 11 SGEDVSDA---SFGS-----KGMNLPASKSVDSGILPDSDYRMIDYPEIGVCVIINN 60
QY 76 KNEPKYTGMCVNGTQKDAALFKCFRSLGPDVIVYNDSCCAKMODLLKKAASEDHNTAA 135
Db 61 KNEHRTGLSSRGTDADASVREVFMKLGKVKVTLNDLSRODLFKLLKNNSEEDHSKRS 120
QY 136 CFCACILLSHGEENVYIGKGVTPKIDLTAFHFGDRCKTLEKPKLFITQACRGTELDIAI 195
Db 121 SFVCVILSHGDEGIFYGTGDPLELKVLTSLFRGDKRSIACKPKLFIQACRGTELDGCI 180
QY 196 QADSGPIINDANPRYKIPVEADFLFAYSTVPGYYSWRSRSGSPFVOALCSILEHGKEI 255
Db 181 EADSGP---DETVCOKIIPVEADFLFAYSTVPGYYSWRSRSGSPFVOALCSILEHGKEI 236
QY 256 LELMQLITRVNDRVARHFEESODDPHFHEKKQIPCVVSMLEKELYF 301
Db 237 LELMQLITRVNDRVARHFEESODDPHFHEKKQIPCVVSMLEKELYF 281

RESULT 5
096ANI PRELIMINARY; PRT; 277 AA.
AC 096ANI;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 31.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC016926; AAH16926.1; -;
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; IL1BCENZME.
DR PROSITE: PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE: PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BCF7FF64A CRC64;

Query Match 44.7%; Score 721; DB 4; Length 277;
Best Local Similarity 50.9%; Pred. No. 6.4e-58;
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSYDAKPDSSFPVLSKSKKNVTMRISIKTRDRVPTYQNNMFEKLGKCIINNKNF 78
Db 5 EDSYDAKPDSSFPVLSKSKKNVTMRISIKTRDRVPTYQNNMFEKLGKCIINNKNF 55
QY 79 DKVTGMYVNGTQKDAALFKCFRSLGPDVIVYNDSCCAKMODLLKKAASEDHNTAACA 138
Db 56 HSTGTMSTRSGTDVDAANLRETFEYVNLKYEVRNKNLDTREIYELMNDVSKEDHSKRSFV 115
QY 139 CILSHGGEENVYIGKGVTPKIDLTAFHFGDRCKTLEKPKLFITQACRGTELDIAIQAD 198
Db 116 CVLHSHGEGIFGNGVPDLAKKINFPFGDKRSITGKPKLFIQACRGTELDGCIEND 175
QY 199 SGPIINDTANPRYKIPVEADFLFAYSTVPGYYSWRSRSGSPFVOALCSILEHGKEI 258
Db 176 SGVDDDMAC---HKIPVEADFLFAYSTVPGYYSWRSRSGSPFVOALCSILEHGKEI 232
QY 259 MQLITRVNDRVARHFEESODDPHFHEKKQIPCVVSMLEKELYF 301
Db 233 MQLITRVNDRVARHFEESODDPHFHEKKQIPCVVSMLEKELYF 275

RESULT 6
095ND5 PRELIMINARY; PRT; 277 AA.
AC 095ND5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Caspase-3.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334413; PubMed=11440638;
RA Muneta Y., Shimofujima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
porcine PK15 cells induced by porcine Fas-ligand".
RL J. Interferon Cytokine Res. 21:409-415(2001).
EMBL: AB029345; BAB55544.1; -;
DR MEROPS: C14.003; -;
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.

Db 121 ---TDEMACQKIPVEADFLYAYSTARGYSWRNSKDSWFIOSLCSMLKLYAHKLOFMH 177

QY 261 ILTRVNDRAVHREESODDPHFHEKKOIPCVSMILTKELIF 301

Db 178 ILTRVNRKVAEFESFSLDSTFPAKKOFCIVSMILTKELIF 218

RESULT 9

093415 PRELIMINARY; PRT; 304 AA.

AC 093415; ID 093415; DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Caspase-6.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20149872; PubMed=10684799;

RA Johnson A.L., Bridgman J.T.;

RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa cells."

RL Biol. Reprod. 62:589-598(2000).

RL [2]

RN SEQUENCE FROM N.A.

RX PubMed=11953316;

RA Ruebhaud S., Korfali N., Villa P., Kottke T.J., Dingwall C., Kaufmann S.H., Earnshaw W.C.;

RT "Caspase-6 gene disruption reveals a requirement for lamin A cleavage in apoptotic chromatin condensation."

RL EMO J. 21:1967-1977(2002).

DR EMBL: AF082329; AAC32378.1;

DR EMBL: AF469049; AAL82386.1;

DR HSSP: P42574; ICP3.

DR MEROPS: C14.005;

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE_P10.

DR InterPro: IPR001309; ICE_P20.

DR Pfam: PF00655; ICE_P10; 1.

DR Pfam: PF00656; ICE_P20; 1.

DR PRINTS: PR00376; ILBCEZYME.

DR SMART: SM00115; CASC. 1.

DR PROSITE: PS01122; CASPASE_CYS. 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SO SEQUENCE 304 AA; 34534 MW; 51CE31EBCAAE7383 CRC64;

Query Match 31.8%; Score 512.5; DB 13; Length 304;

Best Local Similarity 38.1%; Pred. No. 9,1e-39;

Matches 114; Conservative 51; Mismatches 113; Indels 21; Gaps 6;

QY 16 SANEDVDADKPDSSVPSLSFKKKKNTV-MRSIKTRDVRVPTYYNNMFEKLGCIITN 74

Db 9 AAGRVADLSK-----PTTADGNONITEVDAFKRRFRFDEQYKKNHQRGVALIFN 63

QY 75 NKNPKVYGMGVARNCTDADAEALFCFRSLGFDVYIYNDCCSAKMODLLK---ASEEDH 131

Db 64 HEHFFMLRLDRCRTTLDNRNLKRLSLDLDGFEVRIFD---LKAEDVKKVEASRDY 120

QY 132 TNACFACILSHGEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIOACRGTEL 191

Db 121 SNACFCVFLSHGENDVYVYADQIKETITNMFRGDKCSLVGKPKFIITIOACRGDKH 180

QY 192 DDAI-----QADSGPINDT--DANPKYKIPVEADFLFAVSTVPGYSWRNSPGSGMFEV 242

Db 181 DDPLVYDSDVSKETTYNOTEVDAAGYITLPAGADFTMCISVAGGYSHRTVAGSWIT 240

QY 243 QALCSILEHKKELIMQILTRVNDRAVHREESODDPHFHEKKOIPCVSMILTKELIF 301

Db 241 QDLCEALCKHSSLSLEFTELLTVNKRKVSRRYVDCRDINAIGKKOIPCFASMLTKLYF 299

RESULT 10

091866 PRELIMINARY; PRT; 303 AA.

AC 091866; ID 091866; DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Caspase-6.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209426; PubMed=10744739;

RA Nakajima K., Takahashi A., Yeoita Y.;

RT "Structure, expression and function of the Xenopus laevis caspase family."

RL J. Biol. Chem. 275:10484-10491(2000).

DR EMBL: AB038169; BAA94747.1;

DR HSSP: P42574; ICP3.

DR MEROPS: C14.005;

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE_P10.

DR InterPro: IPR001309; ICE_P20.

DR Pfam: PF00655; ICE_P10; 1.

DR Pfam: PF00656; ICE_P20; 1.

DR PRINTS: PR00376; ILBCEZYME.

DR SMART: SM00115; CASC. 1.

DR PROSITE: PS01122; CASPASE_CYS. 1.

DR PROSITE: PS01121; CASPASE_HIS. 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SO SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 31.6%; Score 510; DB 13; Length 303;

Best Local Similarity 37.1%; Pred. No. 1.5e-38;

Matches 108; Conservative 59; Mismatches 106; Indels 18; Gaps 4;

QY 19 EDSVDADKPDSSVPSLSFKKKKNTVRSIKTR--DVRPTYYNNMFEKLGCIITN 76

Db 16 KDSSTASENK-----EOKANVTETDGMTSRTELDPESAERYIMTKRGLALIFNE 66

QY 77 NEDKVTGMGVARNCTDADAEALFCFRSLGFDVYIYNDCCSAKMODLLKKAASEDHNTAC 136

Db 67 DFYQWLRLGSRGRTNTDSMLNRLTLDLGFVQONTYMLRTMDVLEKIOEASTDHSNADC 126

QY 137 FACILSHGEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIOACRGTELDAI- 195

Db 127 FLCVFLSHGDKHIYSYDSIDIDQELINPKGDKCSLVGKPKFIITIOACRGKHDEPVL 186

QY 196 ---QADSGP---INDPDANPKYKIPVEADFLFAVSTVPGYSWRNSPGSGMFEVQALCSIL 249

Db 187 PKDEVSVPLTNTVEVDAASLCTLPAGADFTMCISVAGGYSHRETVAGSWYIODLCAV 246

QY 250 EHGKLEIMQILTRVNDRAVHREESODDPHFHEKKOIPCVSMILTKELIF 300

Db 247 KAVASLEFTEILLTVNKRKVSRRYVDCRDINAIGKKOIPCFASMLTKLIF 297

RESULT 11

091859 PRELIMINARY; PRT; 302 AA.

AC 091859; ID 091859; DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Caspase 6.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laling K.J., Holland J., Bonilla S., Cunningham C., Secombes C.J.;
 RT "Cloning and sequencing of caspase 6 in rainbow trout, *Oncorhynchus*
 RT mykiss, and analysis of its expression under conditions known to
 RT induce apoptosis";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF212219; AAF73848.1;
 DR HSSP: P42574; IPAU.
 DR MEROPS: C14.005;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 302 AA; 34082 MW; 5A6B5F28A0CFA660 CRC64;

Query Match 31.0%; Score 500.5; DB 13; Length 302;
 Best Local Similarity 35.3%; Pred. No. 1.e-37;
 Matches 108; Conservative 50; Mismatches 125; Indels 23; Gaps 4;

OY 3 DDOGAEIIEGVEDSDANEDSVDAKPRDSSFPVSLFSSKKKKVTKRSIKTTDTPVPTQYM 62
 DB 8 DTKGSLKXNKNTSQTGPEBNLETFDGYICSSFSMD-----PAETKYM 51
 OY 63 NEFKAGKCIITINNKNFNDKYTGCVNGTGDADALFKCFRSLGFDVIVYNDSCAKMQL 122
 DB 52 NHKRGGLALIFQEHFPMHLRMPRRNGTADRNGLVRFEDLNFEVQAFDNLKVEEVLQ 111
 OY 123 LKKAEEEDHTNACFACILLSHGEENVYIGKGVTPIKDLTAHFRGDRCTLLEKPLF 182
 DB 112 ISOAEANADADCFVCVSLSHGENDHYAYDKRIADITALEFKDKCKSLVKGKPRIFL 171
 OY 183 IQACRGTELDADAIQ---ADSG-PIND--TDANPRYKIPVEADFLFAYSVPGYYSWRSP 235
 DB 172 IQACRGDKHDDVTPMDVDVSEKTNVEVYVADGVYITLPAAGDFIMCYSAESYISHRET 231
 OY 236 GGSNFVVALCSILEHGELEIMQILTRVNDVRARHFESQSDDPHFHEKKQIPCVSML 295
 DB 232 INGSWYIIDLGCAMRKFGDSLFEFTELLTLVNRKYSMRSGNCDKRAIGKQYPCFASML 291
 OY 296 TKELXF 301
 DB 292 TRKLYF 297

RESULT 12
 OY 077623 PRELIMINARY; PRT; 182 AA.
 AC 077623;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Caspase-3 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rueda B.R., Hendry I.R., Tilly J.L., Hamerlik D.L.;

RT "Accumulation of Caspase-3 mRNA and Induction of Caspase Activity in
 RT the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment in
 RT vivo";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF068837; AAC25713.1;
 DR HSSP: P42574; IPAU.
 DR MEROPS: C14.003;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 FT NON_TER
 SQ SEQUENCE 182 AA; 20408 MW; B5860C6996C21BE7 CRC64;

Query Match 30.6%; Score 493.5; DB 6; Length 182;
 Best Local Similarity 52.8%; Pred. No. 2.e-37;
 Matches 95; Conservative 30; Mismatches 52; Indels 3; Gaps 1;

OY 60 YNNMFEKLGKCIITINNKNFNDKYTGCVNGTGDADALFKCFRSLGFDVIVYNDSCAKM 119
 DB 6 YKMDYPMKGLCIITINNKNFNDKYTGCVNGTGDADALFKCFRSLGFDVIVYNDSCAKM 65
 OY 120 QDLKKAEEEDHTNACFACILLSHGEENVYIGKGVTPIKDLTAHFRGDRCTLLEKPK 179
 DB 66 LELMSDYSKEDHSKRSEFICVLLSHGEGEIIIFGNGVDELKLLASFFRGDCRSLTGKPK 125
 OY 180 LFLIQACRGTELDADAQDSGPTINDANPRYKIPVEADFLFAYSVPGYYSWRSPGCS 239
 DB 126 LFLIQACRGTELDQGLITDGSSEDDMACQ---KIPVEADFLYAVSTAPGYFSWNRKYS 182

RESULT 13
 OY 099M47 PRELIMINARY; PRT; 276 AA.
 AC 099M47;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Caspase 6.
 GN CASP6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002022; AAH02022.1;
 DR HSSP: P42574; IPAU.
 DR MGD: MGI:1312921; Casp6.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 276 AA; 31563 MW; 5965C5932A127B6C CRC64;

Query Match 30.0%; Score 483.5; DB 11; Length 276;
 Best Local Similarity 39.2%; Pred. No. 3.e-36;

[illegible]

RESULT 14					
ID	035397	PRELIMINARY:	PRT:	277 AA.	
AC	035397;				
DT	01-JAN-1998 (TrEMBLrel. 05, Created)				
OC	01-MAR-1998 (TrEMBLrel. 08, Last sequence update)				
DT	01-MAY-2002 (TrEMBLrel. 20, Last annotation update)				
DE	Caspase 6.				
GN	MCH2.				
OS	Rattus norvegicus (Rat).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Rodentia; Sclurognath; Muridae; Murinae; Rattus				
OX	NCBI_TaxID=10116;				
RP	[1]				
RC	SEQUENCE FROM N.A.				
RA	STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY CORTEX;				
RT	Kaushal G.P., Singh A.B., Shah S.V.;				
RL	"Rat kidney Mch2."				
DR	Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: AF025670; AAC25433.1; -				
DR	HSSP: PA2574; IPAU.				
DR	MEROPS: C14.005; -				
DR	InterPro: IPR002398; ICE.				
DR	InterPro: IPR002138; ICE_P10.				
DR	InterPro: IPR001309; ICE_P20.				
DR	Plan: PF00655; ICE_P10; 1.				
DR	Plan: PF00656; ICE_P20; 1.				
DR	PRINTS: PR00376; TLBCEZYME.				
DR	SMART: SM00115; CASC; 1.				
DR	PROSITE: PS01122; CASPASE_CYS; 1.				
DR	PROSITE: PS01121; CASPASE_HIS; 1.				
DR	PROSITE: PS50207; CASPASE_P10; 1.				
DR	PROSITE: PS50208; CASPASE_P20; 1.				
SQ	SEQUENCE 277 AA; 31356 MW; 69D999E729B3BDE2 CRC64;				
Query Match 29.8%; Score 481; DB 11; Length 277;					
Best Local Similarity 38.7%; Pred. No. 6, 2e-36;					
Matches	99; Conservative	43; Mismatches	104; Indels	10; Gaps	
OY	56 PYYQNNNEFKLKCIINNKNFDPKYTGMCVGRNGTDKADEALFKCFRSLSGFDVIYNDCS	115			
DY	16 PAROYMKDHRRKTALFNHERPEFMHIALPERGSTNADRNPNTRRSSELGEVEKCNDLR	75			
OY	116 CAKMODLLKRASSEDPTNACFCFICILLSHREENVYIGKGVPPIKOLTAHFREDCKTLL	175			
DY	76 AEELLKIHIEVSYSSHVADACFLCVPLSHGEGNHIIYAKIETIQTLTGIFKGDKCQSIV	135			
OY	176 EKELFFIOACRSTEED-----DAIQAGSGPINDD--TDANPKRIIVEADFIFYIST	225			
DY	136 GKRIITIIQACRSQHDVLPVLVDVYDHOTDKLDNDVNTGYDAASYTLTPAGADFLMICYSV	195			

OY 226 VGGYSWSPGSGSFWALCSILEEGKLEIMQILRVNDRAVRAREESODDPHHEK 285
||| ||| : | || ||| : : : :
Db 196 AEGYSRHRETVNGSWIYIDDSLMARHOSSLEFTELLTVNRKKSQRVRDPCDPGAIG 255

OY 286 KQIPCVSMLKELXF 301
||| ||| ||| ||| :
Db 256 KQVPEASMLTKKLHF 271

RESULT 15			
Q9BOE7	Q9BOE7	PRELIMINARY:	PRT: 293 AA.
AC Q9BOE7;			
DT 01-JUN-2001 (TrEMBLrel. 17, Created)			
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)			
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)			
DE Caspase 6, apoptosis-related cysteine protease.			
OS Homo sapiens (human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxID=9606;			
[1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=LUNG;			
RA Strausberg R.;			
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RP SEQUENCE FROM N.A.			
RC TISSUE=LUNG;			
RA Strausberg R.;			
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
EMBL: BC004460; AA0460.1; -			
EMBL: BC000305; AA00305.1; -			
HSSP: P42574; IPAU.			
DR MEROPS: C14.005; -			
DR InterPro: IPR002398; ICE.			
DR InterPro: IPR002138; ICE_p10.			
DR InterPro: IPR001309; ICE_p10.			
DR Pfam: PF00655; ICE_p10; 1.			
DR Pfam: PF00656; ICE_p20; 1.			
DR PRINTS: PRO0376; IILBCENZYM.			
DR SMART: SM00115; CASP_1			
DR PROSITE: PS01122; CASPASE_CYS; 1.			
DR PROSITE: PS01121; CASPASE_HIS; 1.			
DR PROSITE: PS50207; CASPASE_P10; 1.			
DR PROSITE: PS50208; CASPASE_P20; 1.			
DR Protease			
Q9 SEQUENCE 293 AA; 33310 MW; 0738AEAF9791EBD7 CRC64;			

[illegible]

Search completed: December 2, 2002, 12:58:10
Job time : 29.7328 secs

XX	01-NOV-1996;	96WO-US17431.
PF		
XX	16-NOV-1995;	95US-0558733.
PR	03-NOV-1995;	95US-0007211.
PR	06-NOV-1995;	95US-0007251.
XX		
PA	(VERT-) VERTEX PHARM INC.	
XX		
PI	Lippke JA, Su M;	
DR	WP1; 1997-272121/24.	
DR	N-PSDB; AAT66970.	
XX		
PT	DNA encoding active, activatable or inactive cysteine protease CMH-1	
PT	for useful in gene therapy for promoting and inhibiting apoptosis and	
XX	for diagnosing cells with potential for apoptosis	
XX		
PS	Claim 3; Page 32-33; 48pp; English.	
XX		
CC	A proenzyme (AAM15247) is activated to CMH-1, or CPp32/Mch2	
CC	homologue-1, a human cysteine protease that is involved in	
CC	apoptosis. Its amino acid sequence was deduced from a full-length	
CC	isolated cDNA clone (AAT66970). Active, activatable (i.e. proenzyme	
CC	or inactivated forms of CMH-1 can be expressed in prokaryotic or	
CC	eukaryotic host cells. The polypeptides are useful for screening	
CC	potential apoptosis inhibitors and for raising antibodies used to	
CC	assay CMH-1, to regulate cholesterol levels, inhibit CMH-1 activity	
CC	and therefore apoptosis, and to purify CMH-1 polypeptides.	
XX		
XX	Sequence 303 AA;	

Query Match	99.6%	Score 1606;	DB 18;	Length 303;
Best Local Similarity	99.3%	Pred. No. 1.4e-161;		
Matches 301; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MADDOGCIIEGQVYDSDANEDSVAKPDRSSVPELSFKKKKNYMRSIKTRDRVPVYYQ	60
Db	1	MADDOGCIIEGQVYDSDANEDSVAKPDRSSVPELSFKKKKNYMRSIKTRDRVPVYYQ	60
QY	61	NNAFEKIGKCIINNKNFVDYVGMGVBNGTDKDAEALFKCFSRIGFVUIYVNDSCAKMQ	120
Db	61	NNAFEKIGKCIINNKNFVDYVGMGVBNGTDKDAEALFKCFSRIGFVUIYVNDSCAKMQ	120
QY	121	DLTKKASEEHTNACACILLSHGEENVYIGKDGWPIINDLTAHFPGDCKTLLKPKL	180
Db	121	DLTKKASEEHTNACACILLSHGEENVYIGKDGWPIINDLTAHFPGDCKTLLKPKL	180
QY	181	FFIOACRGTELDALIOADSGPINDTDANPRYKIPVEADFLFAYSTVGYGYSWRSPGSGW	240
Db	181	FFIOACRGTELDALIOADSGPINDTDANPRYKIPVEADFLFAYSTVGYGYSWRSPGSGW	240
QY	241	FVQALCSIEEHGKELEIMQILTRVNDRVARHSESODDHFHEKKQIPCVVSMLTRKELY	300
Db	241	FVQALCSIEEHGKELEIMQILTRVNDRVARHSESODDHFHEKKQIPCVVSMLTRKELY	300
QY	301	FSQ 303	
Db	301	FSQ 303	

KEY	TERM	DEFINITION	RELEVANCE
RESULT 2	AAAI5262	AAAI5262 standard; Protein; 303 AA.	1
XX	AC	AAAI5262;	1
XX	DT	05-AUG-1997 (first entry)	1
XX	DE	Apoptotic protease Mch3-alpha.	1
XX	XX	Mch3-alpha; cysteine protease; apoptosis; AIDS; ischaemia.	1
XX	XX	neurodegenerative disease; therapy; diagnosis.	1

XX	Homo sapiens.	Location/Qualifiers
OS		
XX		
FH	Key	1..198
FT	Domain	/label= p20
FT		/note= p20 subunit
FT		199..303
FT	Domain	/label= p12
FT		/note= p12 subunit
FT		24..28
FT	Cleavage-site	/label= p20
FT		54..58
FT	Cleavage-site	/label= p17
FT		99..103
FT	Cleavage-site	/label= p12
FT		184..188
FT	Active-site	/note= "QACRG active site"
FT		
PN	WO9718313-A1.	
XX		
PD	22-MAY-1997.	
XX		
PF	12-NOV-1996;	96WO-US18118.
XX		
PR	13-NOV-1995;	95US-0556627.
XX		
PA	(IDUN-) IDUN PHARM INC.	
PA	(UYJE-) UNIV JEFFERSON THOMAS.	
XX		
PI	Alnemri ES, Armstrong R, Fernandes-Alnemri T, Litwack G;	
PI	Tomasetti K;	
XX		
DR	WPI; 1997-289289/26.	
DR	N-PSDB; AAT66992.	
XX		
PT	New gene encoding Mch3, a cysteine protease that regulates apoptosis	
PT	- for treating human diseases associated with apoptosis, and	
PT	screening for antagonists and agonists of Mch3	
XX		
PS	Claim 8; Fig 1; 52pp; English.	
XX		
CC	Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member	
CC	of the interleukin-1-beta converting enzyme (ICE) family of cysteine	
CC	proteases. Its amino acid sequence was deduced from a cDNA clone	
CC	(AAT66992) obt. from a Jukat library. Mch3-beta (AAW15263) has also	
CC	been identified that lacks the active site of Mch3-alpha.	
CC	Mch3-alpha polypeptides can be produced in engineered host cells	
CC	and used to treat human diseases associated with cell death, such	
CC	as AIDS, ischemic injury, neurodegenerative diseases, etc. They	
CC	can also be used to regulate apoptosis and to screen for Mch3	
CC	agonists and antagonists.	
XX		
50	Sequence 303 AA:	

Query Match	99.6%	Score 1606;	DB 18;	Length 303;
Best local Similarity	99.3%	Pred. No. 1.4e-161;		
Matches 301, Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

```
Db 181 FFIQACRGTELDGIGIADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
OY 241 FVOALCSILEEHGKLEIMQILTRVNDRAVARHRESQSDDPHFHEKKQIPCVSMILTREL 300
Db 241 FVOALCSILEEHGKLEIMQILTRVNDRAVARHRESQSDDPHFHEKKQIPCVSMILTREL 300
OY 301 FSO 303
Db 301 FSO 303

RESULT 3
AAV21721
ID AAV21721 standard; Protein; 303 AA.
AC AAV21721;
DT 10-SEP-1999 (first entry)
DE Amino acid sequence of caspase-7 (Mch3).
XX
XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
XX tumour cell; myocardial infarction; human.
XX
XX Homo sapiens.
XX
XX MO9935277-A2.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-US00632.
XX
XX 09-JAN-1998; 98US-0070987.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemut ES;
XX
XX WPI; 1999-419353/35.
XX
XX N-PSDB; AAX81223.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used
XX for screening and identifying inhibitors or enhancers for treating
XX cancer or autoimmune disease
XX
XX PS Disclosure: Fig 17A-B; 74pp; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins
XX after Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAX81217-AAX81226 represent human caspase genes encoding caspase 1-10
XX gene products (AAV21715-Y21724).
XX
XX Sequence 303 AA:
XX
XX Query Match 99.6%; Score 1606; DB 20; Length 303;
XX Best Local Similarity 99.3%; Pred. No. 1.4e-161;
XX Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 61 NMNPEKIGKCIITNNKEDKVTGNGVRNGTDKDAEALFKCPRSLGPDVIYVNDSCAKMQ 120
Db 61 NMNPEKIGKCIITNNKEDKVTGNGVRNGTDKDAEALFKCPRSLGPDVIYVNDSCAKMQ 120
OY 121 DLKKASEEDHTNAACACILLSHGEENVYIGKGVPIKDLTAHFGRDKCTLLERPKL 180
Db 121 DLKKASEEDHTNAACACILLSHGEENVYIGKGVPIKDLTAHFGRDKCTLLERPKL 180
OY 181 FFIQACRGTELDGIGIADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
Db 181 FFIQACRGTELDGIGIADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
OY 241 FVOALCSILEEHGKLEIMQILTRVNDRAVARHRESQSDDPHFHEKKQIPCVSMILTREL 300
Db 241 FVOALCSILEEHGKLEIMQILTRVNDRAVARHRESQSDDPHFHEKKQIPCVSMILTREL 300
OY 301 FSO 303
Db 301 FSO 303

RESULT 4
AAE00604
ID AAE00604 standard; Protein; 303 AA.
XX
XX AAE00604;
XX
XX 02-JUL-2001 (first entry)
XX
XX Human caspase-7.
XX
XX Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Mch3;
XX cysteine protease; apoptosis; caspase expression cassette; metastasis;
XX tumour; cathepsin B; urokinase; proliferation; gene therapy.
XX
XX Homo sapiens.
XX
XX OS
XX FH Key Location/Qualifiers
XX FT Cleavage-site 23..24
XX FT Cleavage-site /label= proteolytic_cleavage_site
XX FT Cleavage-site 198..199
XX FT Cleavage-site /label= proteolytic_cleavage_site
XX FT Cleavage-site 206..207
XX FT Cleavage-site /label= proteolytic_cleavage_site
XX
XX MO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US28941.
XX
XX 20-OCT-1999; 99US-0160559.
XX
XX 14-AUG-2000; 2000US-0225564.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03914.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase
XX subunit, useful for cloning gene encoding enzymes involved in
XX proteolytic cleavage
XX
XX Claim 4; Fig 14; 116pp; English.
XX
XX The present amino acid sequence is human Caspase-7 also known as
XX Interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mch3. Caspases are
XX a family of cysteine proteases, that participate in the initiation and
XX execution of apoptosis. Caspases exist as pro-enzymes, activated by
```

CC cleavage into a large and small subunit, occurring after specific
 CC aspartic acid residues within the pro-enzyme sequence.
 CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in
 CC proteolytic cleavage. An expression cassette containing fusion
 CC polypeptide is used to identify a mutant cell line deficient in an
 CC enzyme of interest and is also useful for diagnosis and suppression of
 CC proliferation or metastases of a tumour cell characterised by
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 CC
 SQ Sequence 303 AA;

Query Match 99.6%; Score 1606; DB 22; Length 303;
 Best Local Similarity 99.3%; Pred. No. 1.4e-161;
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGQVEDSANEDSVAKPDRSSFPVSLFSKKKNVTMSIKTRDRVPYQY 60
 DB 1 MADDGCIIEGQVEDSANEDSVAKPDRSSFPVSLFSKKKNVTMSIKTRDRVPYQY 60
 QY 61 NMNFEKLGKCIITNNKNFQVTGMVNGTGDKADEALFKCFRSLGFPVIYVNDSCAKMQ 120
 DB 61 NMNFEKLGKCIITNNKNFQVTGMVNGTGDKADEALFKCFRSLGFPVIYVNDSCAKMQ 120
 QY 121 DLKKASEEDHTNAACFACILSHGEEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPKL 180
 DB 121 DLKKASEEDHTNAACFACILSHGEEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPKL 180
 QY 181 FTIOACRGTELDGIDQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYISWRSPGSGW 240
 DB 181 FTIOACRGTELDGIDQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYISWRSPGSGW 240
 QY 241 FVOALCSILEEHGKLEIMQILTRVNDVARHFEQSDDPHFEKKOIPCVMMLTKELY 300
 DB 241 FVOALCSILEEHGKLEIMQILTRVNDVARHFEQSDDPHFEKKOIPCVMMLTKELY 300
 QY 301 FSQ 303
 DB 301 FSQ 303

RESULT 5
 ABB01222
 ID ABB01222 standard; Protein; 303 AA.

AC ABB01222;
 XX
 XX 18-SEP-2002 (first entry)

DE Human caspase-7 SEQ ID NO: 24.

DE Human caspase; rev-caspase; gene therapy; protease; apoptosis;
 KW cancer; autoimmune disease; cytostatic; immunosuppressive.

OS Homo sapiens.

PN US6376226-B1.

PD 23-APR-2002.

PF 26-APR-2000; 2000US-0561756.

PR 09-JAN-1998; 98US-070897P.

PR 08-JAN-1999; 99US-0227721.

PR (UYOE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;
 PI
 XX WPI: 2002-451275/48.

DR N-PSDB; ABB03970.

XX New rev-caspases engineered to contain the small subunit fused in frame
 PT N-terminal to the large subunit, which is in reverse order to the wild
 PT type caspases, are useful to treat cancer and autoimmune diseases
 XX
 PS Disclosure; Fig 17; 81pp; English.

XX The present invention provides the protein and coding sequences of human
 CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
 CC can be used in the gene therapy of cancer and autoimmune diseases. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.

SQ Sequence 303 AA;

Query Match 99.6%; Score 1606; DB 23; Length 303;
 Best Local Similarity 99.3%; Pred. No. 1.4e-161;
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGQVEDSANEDSVAKPDRSSFPVSLFSKKKNVTMSIKTRDRVPYQY 60
 DB 1 MADDGCIIEGQVEDSANEDSVAKPDRSSFPVSLFSKKKNVTMSIKTRDRVPYQY 60
 QY 61 NMNFEKLGKCIITNNKNFQVTGMVNGTGDKADEALFKCFRSLGFPVIYVNDSCAKMQ 120
 DB 61 NMNFEKLGKCIITNNKNFQVTGMVNGTGDKADEALFKCFRSLGFPVIYVNDSCAKMQ 120
 QY 121 DLKKASEEDHTNAACFACILSHGEEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPKL 180
 DB 121 DLKKASEEDHTNAACFACILSHGEEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPKL 180
 QY 181 FTIOACRGTELDGIDQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYISWRSPGSGW 240
 DB 181 FTIOACRGTELDGIDQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYISWRSPGSGW 240
 QY 241 FVOALCSILEEHGKLEIMQILTRVNDVARHFEQSDDPHFEKKOIPCVMMLTKELY 300
 DB 241 FVOALCSILEEHGKLEIMQILTRVNDVARHFEQSDDPHFEKKOIPCVMMLTKELY 300
 QY 301 FSQ 303
 DB 301 FSQ 303

RESULT 6
 ABB09297
 ID ABB09297 standard; Protein; 303 AA.

AC ABB09297;

DE 15-JUL-2002 (first entry)

DE Human caspase 7 protein sequence SEQ ID NO:3.

DE Caspase 7; antisense modulation; antiinflammatory; cytostatic;
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
 KW hyperproliferative disorder; cancer; bone metabolism; infection;
 KW cholesterol disorder; inflammation; tumour.

OS Homo sapiens.

PN WO200222640-A1.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US28232.

PR 11-SEP-2000; 2000US-0659860.

XX (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT.
XX WPI: 2002-401902/43.
DR N-PSDB: ABN80825.
XX
PT Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT for modulating gene expression and treating diseases associated with
PT expression of caspase 7 in humans
XX
PS Example 13: Page 94-96; 138pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in
CC length targeted to a nucleic acid molecule encoding caspase 7, which
CC specifically hybridises with and inhibits the expression of caspase 7.
CC (I) has antiinflammatory and cytostatic activities, and can be used in
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC useful for inhibiting the expression of caspase 7 in human cells or
CC tissues, and for treating a human having a disease or condition
CC associated with caspase 7 including inflammatory condition,
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
CC as research reagent and kits. (I) is useful prophylactically to prevent
CC or delay infection, inflammation or tumour formation. The present
CC sequence represents a human caspase 7 protein, which is used in an
CC example from the present invention.
XX
SQ Sequence 303 AA:
Query Match 99.6%; Score 1606; DB 23; Length 303;
Best Local Similarity 99.3%; Pred. No. 1.4e-161;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRSIKTRDRVPYQY 60
DB 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRSIKTRDRVPYQY 60
QY 61 NMNFEKLGKCIITNNKNFDTGTVGVRNGTDXDAEALFKCFRSLGFDVITYNDCSCAKM 120
DB 61 NMNFEKLGKCIITNNKNFDTGTVGVRNGTDXDAEALFKCFRSLGFDVITYNDCSCAKM 120
QY 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPL 180
DB 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPL 180
QY 181 FFIQACRGTELDGAIQADSGPINDTANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
DB 181 FFIQACRGTELDGAIQADSGPINDTANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
QY 241 FVOALCSILIEHGKLEIMQILTRVNDRVARHFEESODDPHFHEKKQIPCVVSMLTKEYL 300
DB 241 FVOALCSILIEHGKLEIMQILTRVNDRVARHFEESODDPHFHEKKQIPCVVSMLTKEYL 300
QY 301 FSQ 303
DB 301 FSQ 303
RESULT 7
ABBO9299
ID ABB09299 standard; Protein: 303 AA.
XX
AC ABB09299;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human caspase 7 protein sequence SEQ ID NO:17.
XX
XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW hyperproliferative disorder; cancer; bone metabolism; infection;

KW cholesterol disorder; inflammation; tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200222640-A1.
XX
XX PD 21-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-0528232.
XX
XX PR 11-SEP-2000; 2000US-0659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI: 2002-401902/43.
DR N-PSDB: ABN80839.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT for modulating gene expression and treating diseases associated with
PT expression of caspase 7 in humans
XX
PS Example 15: Page 101-103; 138pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in
CC length targeted to a nucleic acid molecule encoding caspase 7, which
CC specifically hybridises with and inhibits the expression of caspase 7.
CC (I) has antiinflammatory and cytostatic activities, and can be used in
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC useful for inhibiting the expression of caspase 7 in human cells or
CC tissues, and for treating a human having a disease or condition
CC associated with caspase 7 including inflammatory condition,
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
CC as research reagent and kits. (I) is useful prophylactically to prevent
CC or delay infection, inflammation or tumour formation. The present
CC sequence represents a human caspase 7 protein, which is used in an
CC example from the present invention.
XX
SQ Sequence 303 AA:
Query Match 99.6%; Score 1606; DB 23; Length 303;
Best Local Similarity 99.3%; Pred. No. 1.4e-161;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRSIKTRDRVPYQY 60
DB 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRSIKTRDRVPYQY 60
QY 61 NMNFEKLGKCIITNNKNFDTGTVGVRNGTDXDAEALFKCFRSLGFDVITYNDCSCAKM 120
DB 61 NMNFEKLGKCIITNNKNFDTGTVGVRNGTDXDAEALFKCFRSLGFDVITYNDCSCAKM 120
QY 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPL 180
DB 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLEKPL 180
QY 181 FFIQACRGTELDGAIQADSGPINDTANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
DB 181 FFIQACRGTELDGAIQADSGPINDTANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
QY 241 FVOALCSILIEHGKLEIMQILTRVNDRVARHFEESODDPHFHEKKQIPCVVSMLTKEYL 300
DB 241 FVOALCSILIEHGKLEIMQILTRVNDRVARHFEESODDPHFHEKKQIPCVVSMLTKEYL 300
QY 301 FSQ 303
DB 301 FSQ 303
RESULT 8
ABBO9300

ID	AB093000	Standard: Protein; 336 AA.
XX		
XX	AB093000;	
AC		
XX		
XX		
DT	15-JUL-2002	(first entry)
XX		
XX		
XX		
OS	Homo sapiens.	
XX		
PN	MO200222640-A1.	
XX		
PD	21-MAR-2002.	
XX		
PF	10-SEP-2001; 2001MO-US28232.	
XX		
PR	11-SEP-2000; 2000US-0659860.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
P1	Zhang H, Watt AT;	
XX		
DR	WPI: 2002-401902/43.	
XX		
XX	N-PSDB: ABBN08040.	
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7,	
PT	for modulating gene expression and treating diseases associated with	
XX	expression of caspase 7 in humans	
XX		
XX	Example 15; Page 103-105; 138pp; English.	
CC	The present invention describes a compound (I) 8-50 nucleobases in	
CC	length targeted to a nucleic acid molecule encoding caspase 7, which	
CC	specifically hybridises with and inhibits the expression of caspase 7.	
CC	(I) has antiinflammatory and cytostatic activities, and can be used in	
CC	antisense therapy and as an inhibitor of caspase 7 expression. (I) is	
CC	useful for inhibiting the expression of caspase 7 in human cells or	
CC	tissues, and for treating a human having a disease or condition	
CC	associated with caspase 7 including inflammatory condition,	
CC	hyperproliferative disorder (cancer), or bone metabolism or cholesterol	
CC	disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and	
CC	as research reagent and kits. (I) is useful prophylactically to prevent	
CC	or delay infection, inflammation or tumour formation. The present	
CC	sequence represents a human caspase 7 protein, which is used in an	
CC	example from the present invention.	
XX		
SQ	Sequence	336 AA;
QY	Query Match	99.6%; Score 1606; DB 23; Length 336;
QY	Best Local Similarity	99.3%; Pred. No. 1.6e-16;
Db	Matches 301; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	1	MADDDGCIIEOGVEDSAMEDSVDAKPPDRSSFPSPSLEFSKKKKVMTKSTIKTTRDRVPTQY 60
Db	34	MADDDGCIIEOGVEDSAMEDSVDAKPPDRSSFPSPSLEFSKKKKVMTKSTIKTTRDRVPTQY 93
QY	61	NMNEFKLACKIITINNKNFDKVTYGMVGRNGTGDAALEKFCFSLGFDVIVYNDSCAKMQ 120
Db	94	NMNEFKLACKIITINNKNFDKVTYGMVGRNGTGDAALEKFCFSLGFDVIVYNDSCAKMQ 153
QY	121	DLAKKASEEDTNNACFACIILSHGEENVYIGKDGVPYIKDLTAHFRDRCKTLLKPKL 180
Db	154	DLAKKASEEDTNNACFACIILSHGEENVYIGKDGVPYIKDLTAHFRDRCKTLLKPKL 213
QY	181	FFIOACRTELEDDDAIQADSGPINDPDANPRKIPYEADELFLAYSVTPGYISWRSGRGSW 240
Db	214	FFIOACRTELEDDDAIQADSGPINDPDANPRKIPYEADELFLAYSVTPGYISWRSGRGSW 273

QY	241	FOALCSLILEEHGKELEIMQILTRVNDRAVARHESQSDDPHEHKKOIPCVSMLTRKELY	300
Db	274	FOVALCSLILEEHGKDELMQILTRVNDRAVARHESQSDDPHEHKKOIPCVSMLTRKELY	333
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334	FSQ 336	
QY	301	FSQ 303	
	111		
Db	334	FSQ 336	
QY	341	AA	
	111		
Db	334</		

Db	260	ACRGTELDGIGIQADSGPINDTDANPRYKILPVEADFLFATSTVGYYSWRSRGRGSMFVQA	319
QY	245	LCSTLEEHGKLEIMQIL 262	
Db	320	LCSTLEEHGKLEIMQIL 337	
RESULT 10			
ABAB78588			
ID	ABAB78588	standard; Protein; 303 AA.	
XX			
AC	ABAB78588;		
XX			
DT	15-JUL-2002	(first entry)	
DE	Mouse caspase 7	protein sequence SEQ ID NO:97.	
XX			
KM	Caspase 7;	antisense modulation; antiinflammatory; cytostatic;	
KM	antisense therapy; caspase 7	inhibitor; inflammatory condition;	
KM	hyperproliferative disorder; cancer;	bone metabolism; infection;	
XX	cholesterol disorder; inflammation;	tumour.	
OS	Mus musculus.		
XX			
PN	MO200222640-A1.		
XX			
PD	21-MAR-2002.		
PF	10-SEP-2001; 2001WO-US28232.		
XX			
PR	11-SEP-2000; 2000US-0659860.		
XX			
PA	(ISIS-) ISIS PHARM INC.		
XX			
PI	Zhang H, Watt AT;		
XX			
DR	WPI: 2002-401902/43.		
XX	N-PSDB; ABN80919.		
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7,		
PT	for modulating gene expression and treating diseases associated with		
PT	expression of caspase 7 in humans		
XX			
PS	Example 16; Page 121-123; 138pp; English.		
XX			
CC	The present invention describes a compound (I) 8-50 nucleobases in		
CC	length targeted to a nucleic acid molecule encoding caspase 7, which		
CC	specifically hybridises with and inhibits the expression of caspase 7.		
CC	(I) has antiinflammatory and cytostatic activities, and can be used in		
CC	antisense therapy and as an inhibitor of caspase 7 expression. (I) is		
CC	useful for inhibiting the expression of caspase 7 in human cells or		
CC	tissues, and for treating a human having a disease or condition		
CC	associated with caspase 7 including inflammatory condition,		
CC	hyperproliferative disorder (cancer), or bone metabolism or cholesterol		
CC	disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and		
CC	as research reagent and kits. (I) is useful prophylactically to prevent		
CC	or delay infection, inflammation or tumour formation. The present		
CC	sequence represents a mouse caspase 7 protein, which is used in an		
CC	example from the present invention.		
XX			
XX			
SO	Sequence 303 AA;		
Query Match	83.4%;	Score 1346;	DB 23; Length 303;
Best Local Similarity	81.5%;	Pred. No. 5-2e-134;	
Matches 247;	Conservative 27;	Mismatches 29;	Indels 0; Gaps 0
QY	1	MADGGCTIEGCGVEDSANEDSVDAKPDRRSFFVPSLEFSKRRKKNVYMSIKTTRDRVRPTQY	60
Db	1	MTDDDDCAALEKVEYDSSSEGDVDAKPDRRSIISSITLKKRRNASAGPVRTGRDRVPTLY	60
QY	61	MMNFELKLCITLNNKNPDKVTGAGVNRGTDDDAEALFCCFSLGCDVTVYNDCCSCAKMQ	120
Db	61	RMDFQKMKCKITLNNKNPDKATGMVNRGTDDAGALFCCFONLGEVTVVHNDCCSCAKMQ	120

[illegible]

Query Match	83.4%	Score 1346:	DB 23:	Length 340:
Best Local Similarity	81.5%	Pred. No. 6, 2e-134:		
Matches 247:	Conservative 27:	Mismatches 29:	Indels 0:	Gaps 0:
Qy	1	MADDOGCIEEDGVEDESANEDSVADKAPDRSSFPSPSLFSKKKKVWTRSIKTRDRPTVQY	60	
Db	38	MTDDOCAAELKEKVVSSSESDGVADKPDPRSIISSIIKKKKRNASGPAVTTGDRPPTIY	97	
Qy	61	NNNEFKLKCIIINNNKNNEDKVTGMCVRNGTDAAELFKCFRSLGFVIVYNDSCAMQ	120	
Db	98	RMDFFKMGCCIIINNNKNEFKATGMVRNGTDCAGALFKFCFQNLGFVTVHNDSCAMQ	157	
Qy	121	DLTKRASEDRHTNACCFACIIILSHGEENVYTKGDVTPKLDITAFRGDRCKTLLEKPKL	180	
Db	158	DLTKRASEDRHTNSACFACVILSHGEEDLYKDDVTPKLDITAFRGDRCKTLLEKPKL	217	
Qy	181	FFIQACRGTELDLDAQADSGPINDPANDPRYIPEADBLFAYSTVPGYYSRNRSGRSW	240	
Db	218	FFIQACRGTELDLDAQADSGPINDPANDPRKIPEADBLFAYSTVPGYYSRNRNGKGSW	277	
Qy	241	FVQALCSLIEHKELEIMQILTRVNDRYARHFFESQSDPHHEKKQIPCVASMILTKELY	300	
Db	278	FVQALCSLIEHKELEIMQILTRVNDRYARHFFESQSDPRENEKKQIPCVASMILTKELY	337	
Qy	301	FSQ 303		
Db	338	FSR 340		

RESULT 12
AAB98655
ID AAB98655 standard; protein; 244 AA
XY

[illegible]

RESULT 13
AAW15263
ID AAW15263 standard; Protein; 253 AA

AC AAW15263;

DT 05-AUG-1997 (first entry)

Cysteine protease Mch3-beta.

KW Mch3-beta; cysteine protease; apoptosis; AIDS; ischaemia;

XX
XX

XX

FT	Cleavage-site	24..28

FT	Cleavage-site	54..58
----	---------------	--------

XX 1

XX :
C
C
F
C
C
F
C
F

[illegible][illegible]

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Armstrong R, Fernandes-Alnemri T, Litwack G;

XX
C
C
C
C
C
C

DR N-PSDB; AAT66993.

PT New gene encoding Mch3, a cysteine protease that regulates apoptosis

screening for antagonists and agonists of mch3

PS Claim 8; Fig 1; 52pp; English.

CC Human Mch3-beta (AAW15263) is a novel member of the interleukin-1-

about controlling synthesis of cytochrome P-450s: 133

CC amino acid sequence was deduced from a cDNA clone (AA66993) obtd.
 CC from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneous
 CC alternative splicing events that result in a shift in the reading
 CC frame after amino acid 148 of Mch3-alpha (AAW15262). Mch3-beta does
 CC not include the QACRG active site pentapeptide sequence of
 CC Mch3-alpha. Mch3-beta polypeptides can be produced in engineered
 CC host cells. They can be used as dominant/negative inhibitors of
 CC apoptotic Mch3-alpha to treat or reduce the severity of diseases
 CC characterised by increased programmed cell death, such as AIDS,
 CC ischaemic injury, neurodegenerative diseases, etc., and can also
 CC be used to screen for Mch3 agonists and antagonists.

SO Sequence 253 AA;

Query Match 48.6%; Score 783.5; DB 18; Length 253;
 Best Local Similarity 99.3%; Pred. No. 1.9e-74;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADDOGCIIEOGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVMTSRISKTTDRVPPTYQ 60
 DB 1 MADDOGCIIEOGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVMTSRISKTTDRVPPTYQ 60
 QY 61 NMNFEKLGKCIILNNKNFDKVTGKGVNRTDKDAEALFKCFRSLGFDVIYVNDSCAKMQ 120
 DB 61 NMNFEKLGKCIILNNKNFDKVTGKGVNRTDKDAEALFKCFRSLGFDVIYVNDSCAKMQ 120
 QY 121 DLKKASEEDHTNACFACILLSHGEENV 149
 DB 121 DLKKASEEDHTNACFACILLSHGEENV 149

RESULT 14

ABR78587
 ID ABR78587 standard; Protein; 253 AA.

AC ABR78587;

DT 15-JUL-2002 (first entry)

DE Human caspase 7 protein sequence SEQ ID NO:19.

KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
 KW hyperproliferative disorder; cancer; bone metabolism; infection;
 KW cholesterol disorder; inflammation; tumour.

OS Homo sapiens.

PN WO200222640-A1.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US28232.

PR 11-SEP-2000; 2000US-0659860.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Watt AT;

DR WPI; 2002-401902/43.

DR N-PSDB; ABRN0841.

PT Novel antisense compounds targeted to nucleic acids encoding caspase 7,
 PT for modulating gene expression and treating diseases associated with
 PT expression of caspase 7 in humans

PS Example 15; Page 105-107; 138pp; English.

CC The present invention describes a compound (I) 8-50 nucleobases in
 CC length targeted to a nucleic acid molecule encoding caspase 7, which
 CC specifically hybridises with and inhibits the expression of caspase 7.
 CC (I) has antiinflammatory and cytostatic activities, and can be used in

CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
 CC useful for inhibiting the expression of caspase 7 in human cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with caspase 7 including inflammatory condition,
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
 CC as research reagent and kits. (I) is useful prophylactically to prevent
 CC or delay infection, inflammation or tumour formation. The present
 CC sequence represents a human caspase 7 protein, which is used in an
 CC example from the present invention.

SO Sequence 253 AA;

Query Match 48.6%; Score 783.5; DB 23; Length 253;
 Best Local Similarity 99.3%; Pred. No. 1.9e-74;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADDOGCIIEOGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVMTSRISKTTDRVPPTYQ 60
 DB 1 MADDOGCIIEOGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVMTSRISKTTDRVPPTYQ 60
 QY 61 NMNFEKLGKCIILNNKNFDKVTGKGVNRTDKDAEALFKCFRSLGFDVIYVNDSCAKMQ 120
 DB 61 NMNFEKLGKCIILNNKNFDKVTGKGVNRTDKDAEALFKCFRSLGFDVIYVNDSCAKMQ 120
 QY 121 DLKKASEEDHTNACFACILLSHGEENV 149
 DB 121 DLKKASEEDHTNACFACILLSHGEENV 149

RESULT 15

AAW00372
 ID AAW00372 standard; Protein; 277 AA.

AC AAW00372;

DT 26-JUN-1997 (first entry)

DE Apopain CPP32beta proenzyme.

KW CPP32beta; isoform; inactive; CPP32; proenzyme; cysteine; protease;
 KW proteolytic product; poly(DP-ribose) polymerase; PARP; apopain;
 KW cleavage enzyme; human; monocytic leukaemia; cell line; THP-1;
 KW identification; modulator; recombinant production; gene therapy;
 KW pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody;
 KW antisense DNA; treatment; immune; proliferation; degeneration;
 KW disease; AIDS; acquired immunodeficiency syndrome; autoimmune;
 KW pathogenic infection; cardiovascular; neurological; injury;
 KW alopecia; aging; cancer; type I diabetes; Parkinson's;
 KW Alzheimer's.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX 24-OCT-1996.
 PD
 XX
 PF 17-APR-1996; 96MO-US05282;
 XX
 PR 21-APR-1995; 95US-0426557.
 XX
 PA (MERI) MERCK & CO INC.
 XX (MERI) MERCK FROSST CANADA INC.
 XX
 PI Ali A, Miller DK, Nicholson DW, Thornberry NA, Vailancourt JP;
 XX WPI: 1996-485775/48.
 DR
 XX
 PT Apopain, a new human apoptosis related enzyme - responsible for the
 PT proteolytic breakdown of poly(ADP-ribose) polymerase (PARP) which
 PT occurs at the onset of apoptosis
 XX
 PS Claim 1; Fig 4C; 84pp; English.
 XX
 CC The present sequence is the CPP32beta or Glu190 isoform of the
 CC inactive CPP32 proenzyme (a member of the interleukin converting
 CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of
 CC unknown function cloned from Jurkat cells), the proteolytic product
 CC of which is the poly(ADP-ribose) polymerase (PARP) protease.
 CC Apopain. The PARP cleavage enzyme was purified from the human
 CC monocytic leukaemia cell line, THP-1, using standard ion exchange
 CC chromatography techniques and SDS PAGE. Apopain can be used to
 CC identify apopain activity modulators, while apopain encoding DNA
 CC or ex vivo gene transplantation for enhancing the pro-inflammatory
 CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and
 CC antisense DNA can be used to reduce or eliminate the
 CC pro-inflammatory or pro-apoptotic effects of apopain. Modulation
 CC of apopain activity is beneficial in the treatment of immune,
 CC proliferative and degenerative diseases, e.g. AIDS, autoimmune
 CC disease, pathogenic infections, cardiovascular and neurological
 CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
 CC and Alzheimer's disease.
 CC
 XX
 SQ Sequence 277 AA;
 Query Match 44.7%; Score 721; DB 17; Length 277;
 Best Local Similarity 50.9%; Pred No. 9, 1e-68;
 Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;
 OY 19 EDSVDAKPPDRSSFPSPSLFSKKKKNTMTSRIKTRDRVPTVYQYNNFEKLGKCIINNNKF 78
 DB 5 ENSVDSKSIK-NLEPKRIHSGESMDSGISLDS-----YKMDYFEMGLCIIINNNKF 55
 OY 79 DKVTGMGVANGTDKDAEALFKCFRSLGFVIVYINDSCAKMODLLKASEDHTNAACFA 138
 DB 56 HKSTGMTSRSGTVDVAANLRETFRNLYKEVRNNNDLTREIIVELMRDVSKEHSSKRSFV 115
 OY 139 CILSHGEENVYIKGDTVPIDKLTAFHGRGDRCKTLLKPKLFFIOACRSTELDAIQAD 198
 DB 116 CVLLSHGEGGILFGTNGPVDLKKITNEFRGDRGRSLTGKPKLFIQACRSTELDCGIFTD 175
 OY 199 SGPINDTANPRKIPVEADFLFAYSTVGYYSWRSPGRGSMFVQALCSILBEHGKELET 258
 DB 176 SGVDDDMAC---HKIPVEADFLFAYSTVGYYSWRSPGRGSMFVQALCSILBEHGKELET 232
 OY 259 MOILTRVNDVRAHRESQSDPHFHEKKQIPCVSMLTRKELYF 301
 DB 233 MHILTRVNRKVKATEFEESFSFDATFPAKKQIPCIIVSMLTRKELYF 275

Search completed: December 2, 2002, 12:56:03
 Job time : 34.9569 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:57:12 : Search time 8.35862 Seconds
(Without alignments)
577.252 Million cell updates/sec

Title: US-09-895-263-2

Sequence: 1 MADDCGIEEGVEDSANED.....EKKQIPCVSMLEKLYFSQ 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1613	100.0	303	10	US-09-895-263-2
2	1606	99.6	303	10	US-09-944-851-2
3	1606	99.6	303	10	US-09-954-697-24
4	721	44.7	277	10	US-09-895-263-4
5	718	44.5	277	10	US-09-954-697-12
6	716.5	44.4	264	9	US-10-103-448-3
7	474	29.4	293	10	US-09-954-697-21
8	444.5	27.6	479	10	US-09-952-768-2
9	444.5	27.6	479	10	US-09-954-697-33
10	425.5	26.4	479	10	US-09-410-194-20
11	425.5	26.4	571	10	US-09-410-194-21
12	423.5	26.3	286	10	US-09-862-915-1
13	423.5	26.3	496	10	US-09-952-768-4
14	420.5	26.1	476	10	US-09-954-697-27
15	395	24.5	521	10	US-09-962-834A-2
16	389	24.1	290	10	US-09-954-697-34
17	387	24.0	285	10	US-09-954-697-35
18	372	23.1	503	10	US-09-888-243-29
19	370	22.9	505	10	US-09-888-243-5

20	357.5	22.2	479	10	US-09-888-243-6	Sequence 6, Appli
21	356.5	22.1	416	9	US-10-068-569-1	Sequence 1, Appli
22	347.5	21.5	416	10	US-09-954-697-30	Sequence 30, Appli
23	342	21.2	354	10	US-09-888-243-20	Sequence 20, Appli
24	342	21.2	182	10	US-09-888-243-2	Sequence 2, Appli
25	332.5	20.6	502	10	US-09-809-905-2	Sequence 2, Appli
26	321.5	19.9	167	10	US-09-864-761-48728	Sequence 48728, A
27	317	19.7	435	10	US-09-954-697-9	Sequence 9, Appli
28	308	19.1	451	10	US-09-888-243-28	Sequence 28, Appli
29	300	18.6	163	10	US-09-864-761-47950	Sequence 47950, A
30	264	16.4	52	10	US-09-989-903-40	Sequence 40, Appli
31	264	16.4	81	10	US-09-989-903-35	Sequence 35, Appli
32	263	16.3	300	10	US-09-954-697-36	Sequence 36, Appli
33	258	16.0	242	10	US-09-764-803A-24	Sequence 24, Appli
34	258	16.0	242	10	US-09-845-028-9	Sequence 9, Appli
35	255	15.8	242	10	US-09-845-028-2	Sequence 2, Appli
36	252	15.6	229	10	US-09-764-803A-4	Sequence 4, Appli
37	252	15.6	242	10	US-09-989-903-5	Sequence 5, Appli
38	251.5	15.6	257	10	US-09-764-803A-2	Sequence 2, Appli
39	251.5	15.6	260	10	US-09-989-903-2	Sequence 2, Appli
40	241	14.9	51	10	US-09-989-903-41	Sequence 41, Appli
41	224.5	13.9	410	10	US-09-917-265-24	Sequence 24, Appli
42	221.5	13.7	410	10	US-09-917-265-15	Sequence 15, Appli
43	210	13.0	47	10	US-09-989-903-36	Sequence 36, Appli
44	210	13.0	418	10	US-09-954-697-18	Sequence 18, Appli
45	209	13.0	214	10	US-09-989-903-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-895-263-2
Sequence 2, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PFI40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Db 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTDRVPYQ 60
Qy 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Db 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Qy 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Db 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Qy 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Db 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Qy 301 FSQ 303
Db 301 FSQ 303

RESULT 2

US-09-561-756-24
Sequence 24, Application US/09561756
Patent No. 6376226
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-24

Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTDRVPYQ 60
Db 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTDRVPYQ 60
Qy 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Db 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Qy 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Db 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Qy 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Db 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Qy 301 FSQ 303
Db 301 FSQ 303

RESULT 3
US-09-227-721-24
Sequence 24, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-24

Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTDRVPYQ 60
Db 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTDRVPYQ 60
Qy 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Db 61 NMNFKLGKCIILNNKNDKVTGKVRNGTQKDALEKCRSLGFDVYIYNDSCAKM 120
Qy 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Db 121 DLKASEEDHTNACFACILSHGEENVYIGKGVNPIKDLTAHFRDCKTLEKPKL 180
Qy 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Db 181 FFIQACRGTELDIAIQADSGPIINDTANPRYKIPVEADFLAYSTVPGYSMRSPGRGSW 240
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300
Qy 301 FSQ 303
Db 301 FSQ 303

RESULT 4

US-08-556-627A-2
Sequence 2, Application US/08556627A
Patent No. 6462175
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
APPLICANT: Fernandes-Alnemrl, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch3, A No. 6462175e1 Apoptotic Protease,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Db	181	FFIOACRGELDDGIGQADSGPINDNDANPRYIIPVADLFLAVSTYPGYYSMRSPORGSM	240
QY	241	FVQALCSILIEHKGKLEIMQILTRVNDRYARHFEQSDDPHFEKKQIPCVYSMLTKELY	300
Db	241	FVQALCSILIEHKGKLEIMQILTRVNDRYARHFEQSDDPHFEKKQIPCVYSMLTKELY	300
QY	301	FSQ 303	
Db	301	FSQ 303	
RESULT 4			
US-09-895-263-4			
Sequence 4, Application US/09895263			
Patent No. US20020076793A1			
GENERAL INFORMATION:			
APPLICANT: He, Wei-Wu et al.			
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme			
NUMBER OF SEQUENCES: 12			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Human Genome Sciences, Inc.			
STREET: 9410 Key West Ave.			
CITY: Rockville			
STATE: MD			
COUNTRY: USA			
ZIP: 20850			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/895,263			
FILING DATE: 02-Jul-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: <Unknown>			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: Jonathan L. Klein			
REGISTRATION NUMBER: 41,119			
REFERENCE/DOCKET NUMBER: PFI40			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 301-251-6015			
TELEFAX: 301-309-8439			
INFORMATION FOR SEQ ID NO: 4:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 277 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
US-09-895-263-4			
Query Match 44.7%; Score 721; DB 10; Length 277;			
Best Local Similarity 50.9%; Pred. No. 3.7e-66;			
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;			
QY	19	EDSVADAKDRSSFPVSLPSKKKKNTTMRSIKTRRVRVPTYOYNNANFEKLGKCIINNNKF	78
Db	5	ENSVDYSKSIK-NLEPKIIHGSSEMSMGISLSDS-----YKMDYPEMGLCIIINNNKF	55
QY	79	DKVYGMGVRNGTDKDAEALFKCFRSLGSDVYIYNDSCAKMODLLKASEDHTNAACFA	138
Db	56	HKSTGTMRSRSGDVDAANLRETFRNLKYEVRNKNDLTREIYELMRDVKSEDSKRSSEFV	115
QY	139	CILSHSGEENYIYKGDGTPYIKDLTAHFRGDRCKTLLEPKPLFTIOACRGTELDLAIAD	198
Db	116	CYLLSHGEGEIIIFGNGPVDLKKITINFRGDCRSULTGPKPLFTIOACRGTELDGCIETD	175
QY	199	SGPIINDTANPRYKIIVPADLFLAVSTYPGYYSMRSPORGSMFVQALCSILIEHKGKLEI	258

[illegible]

; INFORMATION FOR SEQ ID NO: 4:

REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 100344

[illegible]

```

; SEQ ID NO 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-20

Query Match      26.4%; Score 425.5; DB 10; Length 479;
Best Local Similarity 35.4%; Pred. No. 1.4e-35;
Matches 112; Conservative 49; Mismatches 114; Indels 41; Gaps 10

QY 9 EEOGVSDSANDSVDAPKPRSSVPSLEFKKKKNVTMR---SKITRDKVPITYQYMMNE 65
DB 179 EEFSEKRS---SLEGSPEFSGEELCGVMTISDSPRODSESQHLDRV---YOMKSK 231
QY 66 KIKGCIITINKNF-----DKVTGKGVNGTDPDKDALELFCKRSIGFVIYVNDSCAK 118
DB 232 PGGYCIITNNHFAKAREKVPKLHSTRDNGNTHLDGALTTTFEELHFEIKPHDDCTVQ 291
QY 119 MODLLKASEEDHTNNAACFACILLSHGEEENVYGNKG-VTPKDLTAHFRGDKTLLK 177
DB 292 IYEILKIYVQLMHSMNDCIFCILLSHGDKGIYGTGQAPAIYEILTSQPTGLKPSLAK 351
QY 178 PLKFLFQACRGDELDAIQADSGPINDTANP-----RKTIPEADPLFVSYV 226
DB 352 PVFVFQACQGNQYKGIPEV---DSEQPLEMDLSSPQTRY-IPDEAFLGLMATV 406
QY 227 PGYVSWRSPGSGMFEVALCSLIEEH-GKELEIMQILTVNDRVARHFPSSODPHFHEK 285
DB 407 NNCVSYRNAREGTVIYQSLCQSLRENCPRGDDILTLTEVN-----YEVSKDKKKNNG 460
QY 286 KOIPCVMKLTLEY 301
DB 461 KQMPQPTFLRKLV 476

RESULT 11
US-09-410-194-21
; Sequence 21, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Iars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 1141-002001
; CURRENT APPLICATION NUMBER: US/09/410.194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-21

Query Match      26.4%; Score 425.5; DB 10; Length 571;
Best Local Similarity 29.9%; Pred. No. 1.7e-35;
Matches 109; Conservative 61; Mismatches 110; Indels 85; Gaps 11;

```

Db 116 CVLLSHGEEGIIIFGTNGPVLKKTITTFNRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
Qy 199 SGPINDTANPRKXIPVEADFLFAFAYSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258
Db 176 SGVDDMAC--HKIPVADADFLAYSTAPGYYSRNSKDSGWFIOQLCAMLKQYADKLEF 232
Qy 259 MQLITRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
Db 233 MHLITRVNKRVAEFEFSFSDATFPAKQIPCIIVSMLTKELYF 275

RESULT 11

US-09-227-721-12
Sequence 12, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emaad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASTSEQ for windows Version 3.0
SEQ ID NO 12
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-12

Query Match 44.5%; Score 718; DB 4; Length 277;
Best Local Similarity 50.5%; Pred. No. 3.5e-73;
Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

Qy 19 EDSVDKPRDSSVPSLFSKSKKKVNTMRSTIKTRDRVPTYQYNNPFELGKCIINKNF 78
Db 5 ENSVDSKSR-NLEPKIIHGSSEMSDGLSDNS-----YKMDYDEMGLCIINKNF 55
Qy 79 DKYTGKGVNRGTGDALEKFCFRSLGFDYIVYNDSCAKMODLLKKAASEDHNAACFA 138
Db 56 HKSTGMSRSGTDVDAANLRETFRNKLYEVNKNNDLREIVELMRVSKEDHSKRSEFV 115
Qy 139 CILLSHGEENVYIGKGVPTPIKDLTAHFNRGDRCKTLLKPKLFIOACRGTELDLDAIOAD 198
Db 116 CVLLSHGEEGIIIFGTNGPVLKKTITTFNRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
Qy 199 SGPINDTANPRKXIPVEADFLFAFAYSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258
Db 176 SGVDDMAC--HKIPVADADFLAYSTAPGYYSRNSKDSGWFIOQLCAMLKQYADKLEF 232
Qy 259 MQLITRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
Db 233 MHLITRVNKRVAEFEFSFSDATFPAKQIPCIIVSMLTKELYF 275

RESULT 12

US-08-983-502-30
Sequence 30, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: YURY V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-30

Query Match 44.5%; Score 718; DB 4; Length 277;
Best Local Similarity 50.5%; Pred. No. 3.5e-73;
Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

Qy 19 EDSVDKPRDSSVPSLFSKSKKKVNTMRSTIKTRDRVPTYQYNNPFELGKCIINKNF 78
Db 5 ENSVDSKSR-NLEPKIIHGSSEMSDGLSDNS-----YKMDYDEMGLCIINKNF 55
Qy 79 DKYTGKGVNRGTGDALEKFCFRSLGFDYIVYNDSCAKMODLLKKAASEDHNAACFA 138
Db 56 HKSTGMSRSGTDVDAANLRETFRNKLYEVNKNNDLREIVELMRVSKEDHSKRSEFV 115
Qy 139 CILLSHGEENVYIGKGVPTPIKDLTAHFNRGDRCKTLLKPKLFIOACRGTELDLDAIOAD 198
Db 116 CVLLSHGEEGIIIFGTNGPVLKKTITTFNRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
Qy 199 SGPINDTANPRKXIPVEADFLFAFAYSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258
Db 176 SGVDDMAC--HKIPVADADFLAYSTAPGYYSRNSKDSGWFIOQLCAMLKQYADKLEF 232
Qy 259 MQLITRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
Db 233 MHLITRVNKRVAEFEFSFSDATFPAKQIPCIIVSMLTKELYF 275

RESULT 13
PCT-US96-10521-30
Sequence 30, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:

```

; GENERAL INFORMATION:
; APPLICANT: Alnemil, Emed S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-954-697-27

Query Match      26.1%; Score 420.5; DB 10; Length 476;
Best Local Similarity 37.4%; Pred. No. 4.4e-35;
Matches 98; Conservative 43; Mismatches 90; Indels 31; Gaps 7;

QY 60 YNNMFEKLGKCIILNNKRF-----DKVTGMGVNCTDKDAEALFKCFRSLGFDVYIN 112
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 223 YOMSKRPGICLIINNHFAKAREKVPRLHSIRONGTHLDAGALTTFEELHFEIKPHH 282

QY 113 DCSGAKMODLLKRSBEDHTNACFACILSHGEENVYIGKD-VTPYIKDLTAHFRGRC 171
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 283 DCTVEQIYEILKIYQMDHSMADCFICILSHGDKGIYTGDEAPLYELTSOFTGLKC 342

QY 172 KTLLEKRLFEITQACRGTELDADAIQADSGPINDTDANP-----RKYIPEADFL 220
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 343 PSLAGKRKVFYIOACQGNVQKGIPIVET---DSEQPYLEMDLSSPQTRV-IPDEADFL 397

QY 221 FAYSTVGYISMRSPGSGMWQALCSLLEH-GKELEIMQILTRVNDRAVHFSQSD 279
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 398 LGMATVNNVCYSYRPADEGTWYIOSLCOSLRERCPRGDILITLLEVN-----YEVSKD 451

QY 280 PHFEKKQIPCVSMITKELF 301
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 452 DKRMGKQMPQPTTLTKKLVF 473

RESULT 15
US-09-962-834A-2
; Sequence 2, Application US/09962834A
; Patent No. US20020034813A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,834A
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,123
; FILING DATE: 1996-07-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

```

```

; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match      24.5%; Score 395; DB 10; Length 521;
Best Local Similarity 30.4%; Pred. No. 2e-32;
Matches 95; Conservative 55; Mismatches 99; Indels 64; Gaps 9;

QY 11 QGVEDSANEDSV-----DAKPDRS-----SEVPSLFSSKKKNVTNRSI--KT 50
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 209 QGEELVSGTDVKTFLFLEALPQESQWKNHAGSNGNRATNGAPSLVSHGMOGASANTINSET 268

QY 51 TDRVPTIYQNNMFEKLGKCIILNNKRPDKVYGMVNRGTDKDAEALFKCFRSLGFDVY 110
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 269 STKRAAVYRMNHNHR--GLCVIVNHSF--TSLKDRGTHKDAEILSHVFWLGFVTHI 323

QY 111 YNDCGAKMODLLKRS--BEDHTNACFACILSHGEENVYIGKD-GVTPYIKDLTAHFRG 168
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 324 HNNVTKEEMVYLOKQKCNPAHADGDCVFICILTHRGFQAVISSDALIPRIMSHFTR 383

QY 169 DRCKTLLKPKLFIQACRGTELDADAIQADSGPINDTD--NPRYKIPVADFLFAYSTV 226
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 384 LQCPRLAEKPKLFIQACGGEIOPSVSLEADALNEQAPTSIQDSIPRPADELLGLATV 443

QY 227 PGYIYMRSPGSGMWQALCSLLEHGELEIMQILTRVNDRAVHFSQSDDPHFEKK 286
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 444 PGYVGFRRHVEESWYIOSLCN-----YEVSKD-----HLKK 468

QY 287 QIPCVSMITKEL 299
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 469 LVPRMLKLEKTM 481

```

Search completed: December 2, 2002, 13:04:18
 Job time : 9.35862 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 14.1052 Seconds
(Without alignments)
632.048 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613
Sequence: 1 MADDOGCIIEQGVDSANED.....EKKQIPCVSMILKELVFSQ 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1613	100.0	303	US-08-462-969B-2	Sequence 2, Appl
2	1606	99.6	303	US-09-561-756-24	Sequence 24, Appl
3	1606	99.6	303	US-09-227-721-24	Sequence 24, Appl
4	1606	99.6	303	US-08-556-627A-2	Sequence 2, Appl
5	721	44.7	277	US-08-591-605-2	Sequence 2, Appl
6	721	44.7	277	US-08-964-308-6	Sequence 6, Appl
7	721	44.7	277	US-08-462-969B-4	Sequence 6, Appl
8	721	44.7	277	US-08-964-313-6	Sequence 6, Appl
9	721	44.7	277	US-09-069-138-6	Sequence 6, Appl
10	718	44.5	277	US-09-561-756-12	Sequence 12, Appl
11	718	44.5	277	US-09-227-721-12	Sequence 12, Appl
12	718	44.5	277	US-08-983-502-30	Sequence 30, Appl
13	718	44.5	277	PCR-US96-10521-30	Sequence 30, Appl
14	711	44.1	277	US-08-964-308-10	Sequence 10, Appl
15	711	44.1	277	US-08-964-313-10	Sequence 10, Appl
16	711	44.1	277	US-09-069-138-10	Sequence 10, Appl
17	709	44.0	277	US-08-890-542A-2	Sequence 2, Appl
18	552	34.2	299	US-08-773-608A-2	Sequence 2, Appl
19	474	29.4	293	US-09-561-756-21	Sequence 21, Appl
20	474	29.4	293	US-09-227-721-21	Sequence 21, Appl
21	468	29.0	278	US-08-522-813-4	Sequence 21, Appl
22	466	28.9	293	US-08-446-923-5	Sequence 5, Appl
23	466	28.9	293	US-09-146-331-5	Sequence 5, Appl
24	466	28.9	293	US-08-896-885-5	Sequence 5, Appl
25	466	28.9	293	US-09-375-256-5	Sequence 5, Appl
26	466	28.9	293	US-08-983-502-31	Sequence 31, Appl
27	466	28.9	293	US-09-376-156-5	Sequence 5, Appl

28	466	28.9	293	5	PCT-US96-10521-31	Sequence 31, Appl
29	444.5	27.6	346	2	US-08-618-408B-2	Sequence 2, Appl
30	444.5	27.6	479	1	US-08-665-220-2	Sequence 2, Appl
31	444.5	27.6	479	4	US-09-291-692-2	Sequence 2, Appl
32	444.5	27.6	479	4	US-09-561-756-33	Sequence 33, Appl
33	444.5	27.6	479	4	US-09-227-721-33	Sequence 27, Appl
34	426.5	26.4	479	4	US-08-983-155-27	Sequence 27, Appl
35	425.5	26.4	479	5	PCT-US96-10521-7	Sequence 12, Appl
36	425.5	26.4	479	5	US-08-807-200-12	Sequence 7, Appl
37	424.5	26.3	479	4	US-09-382-155-26	Sequence 26, Appl
38	424.5	26.3	479	4	US-09-382-155-28	Sequence 26, Appl
39	424.5	26.3	479	4	US-09-001-777-12	Sequence 28, Appl
40	424.5	26.3	479	4	US-09-074-044A-26	Sequence 26, Appl
41	424.5	26.3	479	4	US-09-074-044A-26	Sequence 27, Appl
42	424.5	26.3	479	4	US-09-074-044A-27	Sequence 28, Appl
43	424.5	26.3	479	4	US-09-074-044A-28	Sequence 1, Appl
44	423.5	26.3	389	2	US-08-618-408B-4	Sequence 4, Appl
45	423.5	26.3	389	2	US-08-618-408B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-462-969B-2
Sequence 2, Application US/08462969B
Patent No. 6087150
GENERAL INFORMATION:
APPLICANT: He, Wei-Mu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,969B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF140P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-969B-2
Query Match 100.0%; Score 1613; DB 3; Length 303;
Best local Similarity 100.0%; Pred. No. 1e-174;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MADDOGCIIEQGVDSANEDSDAKPDRSSFPVLSKKNVTMRSIKTRDPVPTYYOY 60
|||||

Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
QY 301 FSQ 303
Db 301 FSQ 303

RESULT 2
US-09-561-756-24 ; Sequence 24, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emaad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-24

Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
QY 301 FSQ 303
Db 301 FSQ 303

RESULT 3
US-09-227-721-24 ; Sequence 24, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emaad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-24

Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDKDAEALFCFSLGFDVIVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGEEENVYIGKDGVTPIKDLTAHFRGRCRTTLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHKGKLEIMQILTRVNDVRAHRESQSDDPHHEKKQIPCVVSMLTKELY 300
QY 301 FSQ 303
Db 301 FSQ 303

RESULT 4
US-08-556-627A-2 ; Sequence 2, Application US/08556627A
; Patent No. 6462175
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emaad S.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/556,627A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-556-627A-2

Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6,4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTRDRVPTTYQ 60
DB 1 MADDGCIIEGVEDSANDSDVDAKPDSSFPVSLFSKKKNVTMRSIKTTRDRVPTTYQ 60
QY 61 MNFELGICIIINNNKFNKVTGMVNGTNDKDAEALFCFRLSGDVYIYNDSCAKKQ 120
DB 61 MNFELGICIIINNNKFNKVTGMVNGTNDKDAEALFCFRLSGDVYIYNDSCAKKQ 120
QY 121 DLTKRASEDHTNACFACILSHGSEENVYIGKGVTPIKDLTAHFRGDRCKTLLEKPKL 180
DB 121 DLTKRASEDHTNACFACILSHGSEENVYIGKGVTPIKDLTAHFRGDRCKTLLEKPKL 180
QY 181 FTIQACRGTELDIAOASGPINDTDANPRKIPVEADFLFAVSTVPGYYSWRSPGRGSW 240
DB 181 FTIQACRGTELDIAOASGPINDTDANPRKIPVEADFLFAVSTVPGYYSWRSPGRGSW 240
QY 241 FVOALCSITIEHGEKELEIMQILTRVNDVRAHRESOSDDPHFEKKOICVYSMLTKELY 300
DB 241 FVOALCSITIEHGEKELEIMQILTRVNDVRAHRESOSDDPHFEKKOICVYSMLTKELY 300
QY 301 FSQ 303
DB 301 FSQ 303

RESULT 5

US-08-591-605-2
Sequence 2, Application US/08591605
Patent No. 6060238
GENERAL INFORMATION:
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,605
FILING DATE: 09-FEB-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-21036.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-605-2

Query Match 44.7%; Score 721; DB 3; Length 277;
Best Local Similarity 50.9%; Pred. No. 1.6e-73;
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSDVADKPDSSFPVSLFSKKKNVTMRSIKTTRDRVPTTYQNNMFKLGKCIINNNKF 78
DB 5 ENSVDSKSIK-NLEPKITHGESMDGSLDNS-----YKMDYEMGICIIINNNKF 55
QY 79 DKVTGMCVRNGTNDKDAEALFCFRLSGEDVYIYNDSCAKKQDLTKRASEDHTNACFA 138
DB 56 HKSTGMSRSGTDVADANLETFRNLYEVNKNKDLTRELVELMRVSKEDHSKRSFV 115
QY 139 CILSHGSEENVYIGKGVTPIKDLTAHFRGDRCKTLLEKPKLFTIQACRGTELDIAO 198
DB 116 CVLSHGSEENVYIGKGVTPIKDLTAHFRGDRCKTLLEKPKLFTIQACRGTELDIAO 175
QY 199 SGPIINDTDANPRKIPVEADFLFAVSTVPGYYSWRSPGRGSWFOALCSITIEHGEKELEI 258
DB 176 SGVDDDMAC---HKIPVEADFLFAVSTVPGYYSWRSPGRGSWFOALCSITIEHGEKELEI 232
QY 259 MQLTRVNDVRAHRESOSDDPHFEKKOICVYSMLTKELY 301
DB 233 MQLTRVNDVRAHRESOSDDPHFEKKOICVYSMLTKELY 275

RESULT 6

US-08-964-308-6
Sequence 6, Application US/08964308
Patent No. 6066715
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-NOV-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-7262
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-6

Query Match	44.7%	Score 721;	DB 3;	Length 277;
Best Local Similarity	50.9%	Pred. No. 1.6e-73;		
Matches 144; Conservative	50;	Mismatches 77;	Indels 12;	Gaps 3;

US-08-462-969B-4
Sequence 4, Application US/08462969B
Patent No. 6087150
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
NUMBER OF INVENTION: Like Apoptosis Protease 3 and 4
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,969B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF140P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-969B-4

```

Query Match 44.7%: Score 721; DB 3; Length 277;
Best Local Similarity 50.9%: Pred. No. 1.6e-73;
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3

RESULT 8
 US-08-964-313-6
 : Sequence 6, Application US/08964313
 : Patent No. 6114132
 :
 : GENERAL INFORMATION:
 : APPLICANT: DESMARAIS, SYLVIE
 : APPLICANT: FRIESEN, RICHARD
 : APPLICANT: GRESSER, MICHAEL
 : APPLICANT: KENNEDY, BRIAN
 : APPLICANT: NICHOLSON, DONALD
 : APPLICANT: RAMACHANDRAN, CHIDAMBARAN
 : APPLICANT: SKOREY, KATHRYN
 : APPLICANT: FORD-HUTCHINSON, ANTHONY
 : TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC
 : STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
 : CITY: RAHWAY
 : STATE: NJ
 : COUNTRY: USA
 : ZIP: 07065
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEO for Windows Version 2.0
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/964,313
 : FILING DATE: 04-NOV-1997
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/030,408
 : FILING DATE: 04-NOV-1996
 : APPLICATION NUMBER: PCT/CA97/00825
 : FILING DATE: 03-NOV-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: DURETTE, PHILIPPE L.
 : REGISTRATION NUMBER: 35,125
 : REFERENCE/DOCKET NUMBER: 19824Y

Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFNRGRDRCSLNGPKLFIIOACRGTELDGIEFTD 175
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGRGSMFWOALCSILIEHKELEI 258
Db 176 SGVDDMAC--HKIPVADDELFAVSTVPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEF 232
QY 259 MQLITRVNDRVARHFEOSODPHHEKQIPCVYSMLTKELYF 301
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

RESULT 11

US-09-227-721-12
Sequence 12, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemat, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 277
TYPE: PRP
ORGANISM: Homo sapien
US-09-227-721-12

Query Match 44.5%; Score 718; DB 4; Length 277;
Best Local Similarity 50.5%; Pred. No. 3.5e-73;

Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDAPDRSSVPSLFSKKKKVNTMRISIKTTDRVPTYOYNNFELGKCIITNNKF 78
Db 5 ENSVDSKSIK-NLEPKIIHGESMSDGSILDNS-----YKMDYPMGICITIIINNKF 55
QY 79 DKVTGKVRNGCTDKDAALFKCFRSLGFDVIVYNDSCAKMODLLKKAESDHTNAACFA 138
Db 56 HKSTGMSRSGTVDANLKRTPFNKLKYEVNKNNDLREIIVELMRDVSKEHDSKRSFV 115
QY 139 CILSHGEENVYIGKDVTPIKDLTAHFRGDRCKTLEKPLFIIOACRGTELDALDIAO 198
Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFNRGRDRCSLNGPKLFIIOACRGTELDGIEFTD 175
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGRGSMFWOALCSILIEHKELEI 258
Db 176 SGVDDMAC--HKIPVADDELFAVSTVPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEF 232
QY 259 MQLITRVNDRVARHFEOSODPHHEKQIPCVYSMLTKELYF 301
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

RESULT 12

US-08-983-502-30
Sequence 30, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: WALLACH-19
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-983-502-30

Query Match 44.5%; Score 718; DB 4; Length 277;
Best Local Similarity 50.5%; Pred. No. 3.5e-73;

Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDAPDRSSVPSLFSKKKKVNTMRISIKTTDRVPTYOYNNFELGKCIITNNKF 78
Db 5 ENSVDSKSIK-NLEPKIIHGESMSDGSILDNS-----YKMDYPMGICITIIINNKF 55
QY 79 DKVTGKVRNGCTDKDAALFKCFRSLGFDVIVYNDSCAKMODLLKKAESDHTNAACFA 138
Db 56 HKSTGMSRSGTVDANLKRTPFNKLKYEVNKNNDLREIIVELMRDVSKEHDSKRSFV 115
QY 139 CILSHGEENVYIGKDVTPIKDLTAHFRGDRCKTLEKPLFIIOACRGTELDALDIAO 198
Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFNRGRDRCSLNGPKLFIIOACRGTELDGIEFTD 175
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGRGSMFWOALCSILIEHKELEI 258
Db 176 SGVDDMAC--HKIPVADDELFAVSTVPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEF 232
QY 259 MQLITRVNDRVARHFEOSODPHHEKQIPCVYSMLTKELYF 301
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

RESULT 13

PCT-US96-10521-30
Sequence 30, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
OPERATING SYSTEM: IBM PC Compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-NOV-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4720
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-10

Query Match 44.1%; Score 711; DB 3; Length 277;
Best Local Similarity 50.5%; Pred. No. 2.2e-72;
Matches 143; Conservative 50; Mismatches 78; Indels 12; Gaps 3;

19 EDSVADKPDSSFPVSLFSKKKKNTMRISIKTRDRVPYQYNNFEKLGKCIINKNF 78
1 EDSVADKPDSSFPVSLFSKKKKNTMRISIKTRDRVPYQYNNFEKLGKCIINKNF 78
5 ENSVDKSKTK-NLEPKIIHSGESMDGSIIDNS-----YKMDYPMGLCIIINKNF 55

79 DKVTGAVRGNTDKDAEALFKCFRSLGFDVIVYNDSCAKMODLLKKAASEDHTNAACA 138
1 DKVTGAVRGNTDKDAEALFKCFRSLGFDVIVYNDSCAKMODLLKKAASEDHTNAACA 138
56 HKSTGTSRSGTDVDANLRETFRNLYEVARNKNDLTREIIVELMRDVSKEDESKRSSFV 115

139 CILSHGEENVYVYKDGVPYPIKDLTAHFRGDRCKTLEKPKLFFIOACRGTELDADIAO 198
1 CILSHGEENVYVYKDGVPYPIKDLTAHFRGDRCKTLEKPKLFFIOACRGTELDADIAO 198
116 CVLLSHGEEGIIIFGTNGPVDLKKITNEFRGDRCSLTGPKFLFIIOACRGTELDGCIETD 175

199 SGPIINDTANPRKIVPEADFLPAYSTVPGYYSWRSPGRSGSWFVQALCSILEHGELEI 258
1 SGPIINDTANPRKIVPEADFLPAYSTVPGYYSWRSPGRSGSWFVQALCSILEHGELEI 258
176 SGVDDDMAC---HKIPVADFLPAYSTAGYYSWRNSKDSGSMFQISLCAMLKQYADKLEF 232

259 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
1 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
233 MHLTRVNRKVAEFESFSDATFPAKKOIPCIIVSMLTKELYF 275

Db 233 MHLTRVNRKVAEFESFSDATFPAKKOIPCIIVSMLTKELYF 275

RESULT 14
US-08-964-308-10
Sequence 10, Application US/08964308
Patent No. 6066715
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: GRESSER, MICHAEL
APPLICANT: KENNEDY, BRIAN
APPLICANT: NICHOLSON, DONALD
APPLICANT: RAMACHANDRAN, CHIDAMBARAN
APPLICANT: SKOREY, KATHRYN
APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
OPERATING SYSTEM: IBM PC Compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-NOV-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4720
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-10

Query Match 44.1%; Score 711; DB 3; Length 277;
Best Local Similarity 50.5%; Pred. No. 2.2e-72;
Matches 143; Conservative 50; Mismatches 78; Indels 12; Gaps 3;

19 EDSVADKPDSSFPVSLFSKKKKNTMRISIKTRDRVPYQYNNFEKLGKCIINKNF 78
1 EDSVADKPDSSFPVSLFSKKKKNTMRISIKTRDRVPYQYNNFEKLGKCIINKNF 78
5 ENSVDKSKTK-NLEPKIIHSGESMDGSIIDNS-----YKMDYPMGLCIIINKNF 55

79 DKVTGAVRGNTDKDAEALFKCFRSLGFDVIVYNDSCAKMODLLKKAASEDHTNAACA 138
1 DKVTGAVRGNTDKDAEALFKCFRSLGFDVIVYNDSCAKMODLLKKAASEDHTNAACA 138
56 HKSTGTSRSGTDVDANLRETFRNLYEVARNKNDLTREIIVELMRDVSKEDESKRSSFV 115

139 CILSHGEENVYVYKDGVPYPIKDLTAHFRGDRCKTLEKPKLFFIOACRGTELDADIAO 198
1 CILSHGEENVYVYKDGVPYPIKDLTAHFRGDRCKTLEKPKLFFIOACRGTELDADIAO 198
116 CVLLSHGEEGIIIFGTNGPVDLKKITNEFRGDRCSLTGPKFLFIIOACRGTELDGCIETD 175

199 SGPIINDTANPRKIVPEADFLPAYSTVPGYYSWRSPGRSGSWFVQALCSILEHGELEI 258
1 SGPIINDTANPRKIVPEADFLPAYSTVPGYYSWRSPGRSGSWFVQALCSILEHGELEI 258
176 SGVDDDMAC---HKIPVADFLPAYSTAGYYSWRNSKDSGSMFQISLCAMLKQYADKLEF 232

259 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
1 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
233 MHLTRVNRKVAEFESFSDATFPAKKOIPCIIVSMLTKELYF 275

Db 233 MHLTRVNRKVAEFESFSDATFPAKKOIPCIIVSMLTKELYF 275

RESULT 15
US-08-964-313-10
Sequence 10, Application US/08964313
Patent No. 6114132
GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: GRESSER, MICHAEL
APPLICANT: KENNEDY, BRIAN
APPLICANT: NICHOLSON, DONALD
APPLICANT: RAMACHANDRAN, CHIDAMBARAN
APPLICANT: SKOREY, KATHRYN
APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19824Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-313-10

Query Match 44.1%; Score 711; DB 3; Length 277;
Best Local Similarity 50.5%; Pred. No. 2,2e-72;
Matches 143; Conservative 50; Mismatches 78; Indels 12; Gaps 3;

QY 19 EDSVDAKPDSSFPVPSLFSSKRRKNTMRISIKTTDRVPTVYQNMNFEKLGKIIINKNF 78
DB 5 ENSYDSKSIK-NLEPKIHGSESMGSLDMS-----YKMDYPMGCLIIINKNF 55
QY 79 DVTGAGVANGTDKDAEALFKCFRSLGFVYIYNDSCAKMODLLKASEDHTNACFA 138
DB 56 HKSTGTSRSGVDVAANLRETFRNKLYEVRNKNDLTREIIVELMRDVSKEHRSRSEV 115
QY 139 CILSHGEENVYIGKGVPIKDLTAHREGDKTILEKPKLFFIOACRSTELDAIAD 198
DB 116 CVLLSHGEGCIIIFGNGPVDLKKITNEFRGDRSLTGKPKLFIIOASRGTELDGIETD 175
QY 199 SGPINDTDANPRKILPVEADFLFAVSTVPGYYSWRSPGRGSMFVOALCSILEHSGKELEI 258
DB 176 SCVDDDMAC---HKIPVEADFLFAVSTVPGYYSWRSPGRGSMFVIOSLCAMLKQYADKLEF 232
QY 259 MQLTRVNDVRAHRESOSDDPHFEKKQIPCVSMLTRELYE 301
DB 233 MHLTRVNRKVALEFESEFSFDATFHAKKQIPCIIVSMLTRELYE 275

Search completed: December 2, 2002, 12:58:44
Job time: 16.1052 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 : Search time 12.8948 Seconds
(without alignments)
632.048 Million cell updates/sec

Title: US-09-895-263-4
Perfect score: 1463

Sequence: 1 MENTENSVDSKSKIKNLEPKI.....AKKQIPCIYSMLTKELFYH 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents-AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1463	100.0	277	3	US-08-591-605-2
2	1463	100.0	277	3	US-08-964-308-6
3	1463	100.0	277	3	US-08-462-969B-4
4	1463	100.0	277	3	US-08-964-313-6
5	1463	100.0	277	4	US-09-069-138-6
6	1460	99.8	277	4	US-09-561-756-12
7	1460	99.8	277	4	US-09-227-721-12
8	1460	99.8	277	4	US-08-983-502-30
9	1460	99.8	277	5	PCT-US96-10521-30
10	1453	99.3	277	3	US-08-964-308-10
11	1453	99.3	277	3	US-08-964-313-10
12	1453	99.3	277	4	US-09-069-138-10
13	1304	89.1	277	2	US-08-890-542A-2
14	912	62.3	290	4	US-09-561-756-34
15	912	62.3	290	4	US-09-227-721-34
16	896	61.2	285	4	US-09-561-756-35
17	896	61.2	285	4	US-09-561-756-35
18	761	52.0	148	3	US-08-964-308-11
19	761	52.0	148	4	US-08-964-313-11
20	761	52.0	148	4	US-09-069-138-11
21	725	49.6	303	4	US-09-561-756-24
22	725	49.6	303	4	US-09-227-721-24
23	725	49.6	303	4	US-08-556-627A-2
24	721	49.3	293	3	US-08-462-969B-2
25	525.5	35.9	293	4	US-09-561-756-21
26	525.5	35.9	293	4	US-09-227-721-21
27	517.5	35.4	293	1	US-08-446-925-5

28	517.5	35.4	293	2	US-09-146-331-5	Sequence 5, Appl
29	517.5	35.4	293	2	US-08-896-885-5	Sequence 5, Appl
30	517.5	35.4	293	4	US-09-375-256-5	Sequence 5, Appl
31	517.5	35.4	293	4	US-08-983-502-31	Sequence 31, Appl
32	517.5	35.4	293	4	US-09-376-156-5	Sequence 5, Appl
33	517.5	35.4	293	5	PCT-US96-10521-31	Sequence 31, Appl
34	516.5	35.3	278	3	US-08-522-813-4	Sequence 4, Appl
35	470	32.1	299	2	US-08-773-608A-2	Sequence 2, Appl
36	429	29.3	476	4	US-09-561-756-27	Sequence 27, Appl
37	429	29.3	476	4	US-09-227-721-27	Sequence 27, Appl
38	423	28.9	286	4	US-09-360-017-1	Sequence 1, Appl
39	421	28.8	389	2	US-08-618-408B-4	Sequence 4, Appl
40	421	28.8	464	4	US-08-983-502-7	Sequence 4, Appl
41	421	28.8	464	5	PCT-US96-10521-18	Sequence 18, Appl
42	421	28.8	479	4	US-08-983-502-7	Sequence 18, Appl
43	421	28.8	479	5	PCT-US96-10521-7	Sequence 7, Appl
44	421	28.8	496	1	US-08-665-220-4	Sequence 4, Appl
45	421	28.8	496	4	US-09-291-692-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-591-605-2
Sequence 2, Application US/08591605
Patent No. 6060238
GENERAL INFORMATION:
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,605
FILING DATE: 09-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-21036.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-605-2

Query Match 100.0%; Score 1463; DB 3; Length 277;
Best local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDSKSKIKNLEPKIHGSESDGSIISDNYSKMDYPMGICITINNNKHFHSTG 60
|||||
DB 1 MENTENSVDSKSKIKNLEPKIHGSESDGSIISDNYSKMDYPMGICITINNNKHFHSTG 60
|||||
QY 61 MRSRGTDAANLRETFNLKYEVRNKNLDTREIEIYELRADVSKEDHSKRSSFVCVLLS 120

Db 61 MTSSSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEHSSKSSFCVLLS 120
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESFSDATFHAKKOIPCIVSMLTKELFYH 277
Db 241 RKVATEFESFSDATFHAKKOIPCIVSMLTKELFYH 277

RESULT 2

US-08-964-308-6
; Sequence 6, Application US/08964308
; Patent No. 6066715
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: ZAMBONI, ROBERT
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
; TITLE OF INVENTION: BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-964-308-6

Query Match 100.0%; Score 1463; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,7e-161;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDSSIKNLEPKIIHGSSEMSDGSISLDSYKMDYEMGLCIIINKNKFKSTG 60
Db 1 MENTENSVDSSIKNLEPKIIHGSSEMSDGSISLDSYKMDYEMGLCIIINKNKFKSTG 60
QY 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEHSSKSSFCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEHSSKSSFCVLLS 120
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180

Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESFSDATFHAKKOIPCIVSMLTKELFYH 277
Db 241 RKVATEFESFSDATFHAKKOIPCIVSMLTKELFYH 277

RESULT 3

US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,969B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,251
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PFI40P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-969B-4

Query Match 100.0%; Score 1463; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,7e-161;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDSSIKNLEPKIIHGSSEMSDGSISLDSYKMDYEMGLCIIINKNKFKSTG 60
Db 1 MENTENSVDSSIKNLEPKIIHGSSEMSDGSISLDSYKMDYEMGLCIIINKNKFKSTG 60
QY 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEHSSKSSFCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEHSSKSSFCVLLS 120
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240

|||||
Db 181 DMACHRIPEADFLVAYSTAPGYISWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
QY 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELYFYH 277
Db 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELYFYH 277

RESULT 4
US-08-964-313-6
Sequence 6, Application US/08964313
Patent No. 6114132

GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: GRESSER, MICHAEL
APPLICANT: KENNEDY, BRIAN
APPLICANT: NICHOLSON, DONALD
APPLICANT: RAMACHANDRAN, CHIDAMBARAN
APPLICANT: SKOREY, KATHRYN
APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964, 313
FILING DATE: 04-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19824Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-313-6

Query Match 100.0%; Score 1463; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENTENSVDKSIKLEPKIIHGSSEMDGSLDMSYKMDYPEMGLCTIIINKNFHKSTG 60
Db 1 MENTENSVDKSIKLEPKIIHGSSEMDGSLDMSYKMDYPEMGLCTIIINKNFHKSTG 60
QY 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDYSKEDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDYSKEDHSKRSSFVCVLLS 120

QY 121 HGESEITGTGPNVPDLKTTNFFRGDRCSLTGKRKPLFIQACRGTELDGCIETDGVDD 180
Db 121 HGESEITGTGPNVPDLKTTNFFRGDRCSLTGKRKPLFIQACRGTELDGCIETDGVDD 180
QY 181 DMACHRIPEADFLVAYSTAPGYISWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
Db 181 DMACHRIPEADFLVAYSTAPGYISWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
QY 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELYFYH 277
Db 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELYFYH 277

RESULT 5
US-09-069-138-6
Sequence 6, Application US/09069138
Patent No. 6348572

GENERAL INFORMATION:
APPLICANT: DESMARAIS, SYLVIE
APPLICANT: DUFRESNE, CLAUDE
APPLICANT: FRIESEN, RICHARD
APPLICANT: LEBLANC, YVES
APPLICANT: ROY, PATRICK
APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMONTI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069, 138
FILING DATE: 29-APR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19840Y1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-069-138-6

Query Match 100.0%; Score 1463; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENTENSVDKSIKLEPKIIHGSSEMDGSLDMSYKMDYPEMGLCTIIINKNFHKSTG 60
Db 1 MENTENSVDKSIKLEPKIIHGSSEMDGSLDMSYKMDYPEMGLCTIIINKNFHKSTG 60
QY 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDYSKEDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIIVELMRDYSKEDHSKRSSFVCVLLS 120

APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-30

Query Match 99.8%; Score 1460; DB 4; Length 277;
Best Local Similarity 99.6%; Pred. No. 3.7e-161;
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDGSLDINSYKMDYPEMGLCIINNNKPHKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDGSLDINSYKMDYPEMGLCIINNNKPHKSTG 60
QY 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCVLLS 120
DB 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCVLLS 120
QY 121 HGEGLIFGTNGPVLDKLTITNFRGDRCSLTGKPKLFIIOACRGTETDCCGIEETDSGVD 180
DB 121 HGEGLIFGTNGPVLDKLTITNFRGDRCSLTGKPKLFIIOACRGTETDCCGIEETDSGVD 180
QY 181 DMACHRIPEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
DB 181 DMACHRIPEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
QY 241 RYVATEFESEFSDATFHAKKOIPCIIVSMLTRELYFYH 277
DB 241 RYVATEFESEFSDATFHAKKOIPCIIVSMLTRELYFYH 277

RESULT 9
PCT-US96-10521-30
Sequence 30, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-30

Query Match 99.8%; Score 1460; DB 5; Length 277;
Best Local Similarity 99.6%; Pred. No. 3.7e-161;
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDGSLDINSYKMDYPEMGLCIINNNKPHKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDGSLDINSYKMDYPEMGLCIINNNKPHKSTG 60
QY 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCVLLS 120
DB 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCVLLS 120
QY 121 HGEGLIFGTNGPVLDKLTITNFRGDRCSLTGKPKLFIIOACRGTETDCCGIEETDSGVD 180
DB 121 HGEGLIFGTNGPVLDKLTITNFRGDRCSLTGKPKLFIIOACRGTETDCCGIEETDSGVD 180
QY 181 DMACHRIPEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
DB 181 DMACHRIPEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKOYADKLEFMHILTRVN 240
QY 241 RYVATEFESEFSDATFHAKKOIPCIIVSMLTRELYFYH 277
DB 241 RYVATEFESEFSDATFHAKKOIPCIIVSMLTRELYFYH 277

RESULT 10
US-08-964-308-10
Sequence 10, Application US/08964308
Patent No. 6066715
GENERAL INFORMATION:
APPLICANT: DESARNAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILING DATE: 04-NOV-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 19840 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-7262
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-308-10

Query Match 99.3%; Score 1453; DB 3; Length 277;
Best Local Similarity 99.6%; Pred. No. 2.4e-160;
Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGLCIINNNKFKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGLCIINNNKFKSTG 60
QY 61 MTSRSGTDVAANLRETFRNLYEVNKNNDLTREIYELMRDYSKEDHSKRSFVCVLLS 120
DB 61 MTSRSGTDVAANLRETFRNLYEVNKNNDLTREIYELMRDYSKEDHSKRSFVCVLLS 120
QY 121 HGEGLIFGTNGPVDLKKITNFRGDRCSLTGPKLFTIOACRGTELDGIEITDSGVD 180
DB 121 HGEGLIFGTNGPVDLKKITNFRGDRCSLTGPKLFTIOASRGTELDGIEITDSGVD 180
QY 181 DMACKRIPVADFLYASTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
DB 181 DMACKRIPVADFLYASTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277
DB 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277

RESULT 11

US-08-964-313-10
Sequence 10, Application US/08964313
Patent No. 6114132

GENERAL INFORMATION:

APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: GRESSER, MICHAEL
APPLICANT: KENNEDY, BRIAN
APPLICANT: NICHOLSON, DONALD
APPLICANT: RAMACHANDRAN, CHIDAMBARAN
APPLICANT: SKOREY, KATHRYN
APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,408

FILING DATE: 04-NOV-1996

APPLICATION NUMBER: PCT/CA97/00825

FILING DATE: 03-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: DURETTE, PHILIPPE L.

REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19824Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-4568
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-313-10

Query Match 99.3%; Score 1453; DB 3; Length 277;
Best Local Similarity 99.6%; Pred. No. 2.4e-160;
Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGLCIINNNKFKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGLCIINNNKFKSTG 60
QY 61 MTSRSGTDVAANLRETFRNLYEVNKNNDLTREIYELMRDYSKEDHSKRSFVCVLLS 120
DB 61 MTSRSGTDVAANLRETFRNLYEVNKNNDLTREIYELMRDYSKEDHSKRSFVCVLLS 120
QY 121 HGEGLIFGTNGPVDLKKITNFRGDRCSLTGPKLFTIOACRGTELDGIEITDSGVD 180
DB 121 HGEGLIFGTNGPVDLKKITNFRGDRCSLTGPKLFTIOASRGTELDGIEITDSGVD 180
QY 181 DMACKRIPVADFLYASTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
DB 181 DMACKRIPVADFLYASTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277
DB 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277

RESULT 12

US-09-069-138-10
Sequence 10, Application US/09069138
Patent No. 6348572

GENERAL INFORMATION:

APPLICANT: DESMARAIS, SYLVIE
APPLICANT: DURESNE, CLAUDE
APPLICANT: FRIESEN, RICHARD
APPLICANT: LEBLANC, YVES
APPLICANT: ROY, PATRICK
APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,138

FILING DATE: 29-APR-1998

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: DURETTE, PHILIPPE L.

REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19840YIA

TELECOMMUNICATION INFORMATION:


```

; Sequence 34, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemi, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Rev-Caspase-3 constructed from human caspase -3
US-09-227-721-34

```

```

Query Match      62.3%; Score 912; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MENTENSVDKSTKLNLEPKIIHSESMDSGISLDNSYKMDYPEKGLCIINNNKHFHSTG 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 116 MENTENSVDKSTKLNLEPKIIHSESMDSGISLDNSYKMDYPEKGLCIINNNKHFHSTG 175
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 MTSRSGTDVDAANLRETFRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCLLS 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 176 MTSRSGTDVDAANLRETFRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCLLS 235
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 HSEGIIFGTNGPVDLKKITNFFRGDRCSLTGPKLFTIOACRGTELDCGIETD 175
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 236 HGBEGIIIFGTNGPVDLKKITNFFRGDRCSLTGPKLFTIOACRGTELDCGIETD 290
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Search completed: December 2, 2002, 12:58:44
 Job time : 12.8948 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:57:12 ; Search time 7.64138 Seconds
(Without alignments)
577.252 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463

Sequence: 1 MENTENSVDKSIKMLEPKI.....AKQIPCIYSMLTKELFYH 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/PCT07_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1463	100.0	277	10	US-09-895-263-4
2	1460	99.8	277	10	US-09-954-697-12
3	1397	95.5	264	9	US-10-103-448-3
4	912	62.3	290	10	US-09-954-697-34
5	896	61.2	285	10	US-09-954-697-35
6	833	56.9	182	10	US-09-809-905-2
7	725	49.6	303	10	US-09-944-851-2
8	725	49.6	303	10	US-09-954-697-24
9	721	49.3	303	10	US-09-895-263-2
10	525.5	33.9	293	10	US-09-954-697-21
11	429	28.3	476	10	US-09-954-697-27
12	423	28.9	286	10	US-09-862-915-1
13	421	28.8	479	10	US-09-410-194-20
14	421	28.8	496	10	US-09-952-768-4
15	417	28.5	416	9	US-10-068-569-1
16	411	28.1	416	10	US-09-954-697-30
17	376.5	25.7	503	10	US-09-888-243-29
18	374.5	25.6	505	10	US-09-888-243-5
19	372.5	25.5	479	10	US-09-888-243-6

20	349	23.9	479	10	US-09-952-768-2	Sequence 2, Appli
21	349	23.9	479	10	US-09-954-697-33	Sequence 33, Appli
22	343.5	23.5	354	10	US-09-888-243-20	Sequence 20, Appli
23	343.5	23.5	503	10	US-09-888-243-2	Sequence 2, Appli
24	336.5	23.0	451	10	US-09-888-243-28	Sequence 28, Appli
25	328.5	22.5	435	10	US-09-954-697-9	Sequence 9, Appli
26	321	21.9	521	10	US-09-962-834A-2	Sequence 2, Appli
27	321	21.9	571	10	US-09-410-194-21	Sequence 21, Appli
28	316	21.6	167	10	US-09-864-761-48728	Sequence 48728, A
29	294	20.1	300	10	US-09-954-697-36	Sequence 36, Appli
30	274.5	18.8	242	10	US-09-764-803A-24	Sequence 24, Appli
31	274.5	18.8	242	10	US-09-845-028-2	Sequence 2, Appli
32	274.5	18.8	242	10	US-09-845-028-9	Sequence 9, Appli
33	274	18.7	257	10	US-09-764-803A-2	Sequence 2, Appli
34	274	18.7	260	10	US-09-989-903-2	Sequence 2, Appli
35	273.5	18.7	242	10	US-09-989-903-5	Sequence 5, Appli
36	271.5	18.6	229	10	US-09-764-803A-4	Sequence 4, Appli
37	265.5	18.1	410	10	US-09-917-265-24	Sequence 24, Appli
38	259.5	17.7	410	10	US-09-917-265-15	Sequence 15, Appli
39	250	17.1	51	10	US-09-989-903-34	Sequence 34, Appli
40	247.5	16.9	402	10	US-09-888-243-14	Sequence 14, Appli
41	246.5	16.8	377	10	US-09-954-697-15	Sequence 15, Appli
42	244	16.7	58	10	US-09-989-903-27	Sequence 27, Appli
43	240.5	16.4	163	10	US-09-864-761-47950	Sequence 47950, A
44	232.5	15.9	418	10	US-09-954-697-18	Sequence 18, Appli
45	229.5	15.7	214	10	US-09-989-903-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-895-263-4
Sequence 4, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Db 116 MENTENSVDKSKIKNLEPKIIGHSESMDSGISLDSYKMDYPMGLCIITINKNFHKSTG 175
QY 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 120
Db 176 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 235
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
Db 236 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 290

RESULT 5

US-09-954-697-35
Sequence 35, Application US/09954697
Patent No. US20020106631A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
FILE REFERENCE: 480140.43ID2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 285
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Uncleavable Rev-Caspase-3 constructed from human
US-09-954-697-35

Query Match 61.2%; Score 896; DB 10; Length 285;
Best Local Similarity 98.9%; Pred. No. 7.9e-81;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIGHSESMDSGISLDSYKMDYPMGLCIITINKNFHKSTG 60
Db 111 MENTENSVDKSKIKNLEPKIIGHSESMDSGISLDSYKMDYPMGLCIITINKNFHKSTG 170
QY 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 120
Db 171 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 230
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
Db 231 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 285

RESULT 6

US-09-809-905-2
Sequence 2, Application US/09809905
Patent No. US2002001806A1
GENERAL INFORMATION:
APPLICANT: Huang, Yuanhui
APPLICANT: Sun, Yi
APPLICANT: Wang, Kevin Ka-Wang
TITLE OF INVENTION: CASPASE-35 SPLICING VARIANT
FILE REFERENCE: U.S. Application A0000224
CURRENT APPLICATION NUMBER: US/09/809,905
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/204,468
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-09-809-905-2

Query Match 56.9%; Score 833; DB 10; Length 182;

Best Local Similarity 100.0%; Pred. No. 6.8e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIGHSESMDSGISLDSYKMDYPMGLCIITINKNFHKSTG 60
Db 1 MENTENSVDKSKIKNLEPKIIGHSESMDSGISLDSYKMDYPMGLCIITINKNFHKSTG 60
QY 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFVCVLLS 120
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIO 161
Db 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIO 161

RESULT 7

US-09-944-851-2
Sequence 2, Application US/09944851
Patent No. US20020102648A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin
TITLE OF INVENTION: Mch3, A No. US20020102648A1 Apoptotic Protease,
Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-851-2

Query Match 49.6%; Score 725; DB 10; Length 303;
Best Local Similarity 51.2%; Pred. No. 6.1e-64;
Matches 145; Conservative 49; Mismatches 77; Indels 12; Gaps 3;

QY 5 ENSVDKSKIK-NLEPKIIGHSESMDSGISLDSN-----YKMDYPMGLCIITINKNF 55
Db 19 EDSVDKPKDRSSFPVPSLFSKSKKKNVTMRISIKTTRDVPYQYNNMFELGCIITINKNF 78
QY 56 HKSTGMSRSGTDVDAANLRETFRNLYKEVRNKNDLTREIYELMRDVSKEHRSKRSFV 115

```
Db 79 DRYTGMGVRNKTDAEALFKCFRSLGFDVLYVYDCCAGKMODLLKKAASEDH7NAACFA 138
OY 116 CULLSHGEEGIIIFGTNGPVDLKKITNFERGDRCSLTGPKLFTIQAACRGTELDGCIETD 175
Db 139 CILLSHGEEENVYKGDVTPKIDLTAFHGRDRCKTLEKPKLFTIQAACRGTELDGCIAD 198
OY 176 SGVDDMAC---HKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEF 232
Db 199 SGPIINDDANPRKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEI 258
OY 233 MHILTRVNRKATFEESFSDATFHAKKOIPCIYSMLTKELF 275
Db 259 MQLTRVNDRAVRAHFESQSDPHFHEKKOIPCVVSMLTKELYF 301
```

RESULT 8
US-09-954-697-24

```
; Sequence 24, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-24
```

```
Query Match 49.6%; Score 725; DB 10; Length 303;
Best Local Similarity 51.2%; Pred. No. 6,1e-64;
Matches 145; Conservative 49; Mismatches 77; Indels 12; Gaps 3;
```

```
OY 5 ENSVDSKSIK-NLEPKTIHSESDSGISLDS-----YKMDYEMGCIITINKNF 55
Db 19 EDSDVDAKPPDRSSVPSLFSKSKKNVNTMRISIKITDRVPTIYQNNFELGKCIITINKNF 78
OY 56 HKSTGMSRSGTDVDAANLRETFRNLYEVNRKNDLTREELVELMRDYSKEDSKRSSFV 115
Db 79 DKVTGMGVRNKTDAEALFKCFRSLGFDVLYVYDCCAGKMODLLKKAASEDH7NAACFA 138
OY 116 CULLSHGEEGIIIFGTNGPVDLKKITNFERGDRCSLTGPKLFTIQAACRGTELDGCIETD 175
Db 139 CILLSHGEEENVYKGDVTPKIDLTAFHGRDRCKTLEKPKLFTIQAACRGTELDGCIAD 198
OY 176 SGVDDMAC---HKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEF 232
Db 199 SGPIINDDANPRKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEI 258
OY 233 MHILTRVNRKATFEESFSDATFHAKKOIPCIYSMLTKELF 275
Db 259 MQLTRVNDRAVRAHFESQSDPHFHEKKOIPCVVSMLTKELYF 301
```

RESULT 9
US-09-895-263-2

```
; Sequence 2, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
```

```
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PFI40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-263-2
```

```
Query Match 49.3%; Score 721; DB 10; Length 303;
Best Local Similarity 50.9%; Pred. No. 1.5e-63;
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;
```

```
OY 5 ENSVDSKSIK-NLEPKTIHSESDSGISLDS-----YKMDYEMGCIITINKNF 55
Db 19 EDSDVDAKPPDRSSVPSLFSKSKKNVNTMRISIKITDRVPTIYQNNFELGKCIITINKNF 78
OY 56 HKSTGMSRSGTDVDAANLRETFRNLYEVNRKNDLTREELVELMRDYSKEDSKRSSFV 115
Db 79 DKVTGMGVRNKTDAEALFKCFRSLGFDVLYVYDCCAGKMODLLKKAASEDH7NAACFA 138
OY 116 CULLSHGEEGIIIFGTNGPVDLKKITNFERGDRCSLTGPKLFTIQAACRGTELDGCIETD 175
Db 139 CILLSHGEEENVYKGDVTPKIDLTAFHGRDRCKTLEKPKLFTIQAACRGTELDGCIAD 198
OY 176 SGVDDMAC---HKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEF 232
Db 199 SGPIINDDANPRKIPVADFLVAYSTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADKLEI 258
OY 233 MHILTRVNRKATFEESFSDATFHAKKOIPCIYSMLTKELF 275
Db 259 MQLTRVNDRAVRAHFESQSDPHFHEKKOIPCVVSMLTKELYF 301
```

RESULT 10
US-09-954-697-21

```
; Sequence 21, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 293
; TYPE: PRT
```


ORGANISM: Homo sapiens
us-09-410-194-20

Query Match 28.8%; Score 421; DB 10; Length 479;
Best Local Similarity 37.8%; Pred. No. 1e-33;
Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;

QY 24 SESMDSGISLDNSYKMDYEMGICITIIINKNFKHST-----GMSRSRGTDVDAANLRE 76
DB 217 SESQ-----TLDKYOMKSRPGCYCLIIINNHNFAKAREKVPKLSIRDRNGTHLDAGALLT 272
QY 77 TFRNLKYEVRNKNDLTREETVELMRDYSKEDHSKSSFCVLLSHGEGIIIFGTNG--PVD 135
DB 273 TFEELHFEIRPHDCTVEQIYEILKIYOLMDHSMDCFCIIISHGDKGIITGDOGEAP 332
QY 136 LKKTINFEPRDRSLTGKPKLFIIOACRGTELDGCI--ETDSC-----VDDMACHK--- 186
DB 333 IYELTSQFTGLKCPSLAGKPKVFFIOACQGDNYOKGIPVETDSEOPYLEMDLSSPQTRY 392
QY 187 IPEADFLVAYSTAPGYYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNRKVAT 245
DB 393 IPDEADFLGMATVNNCVSRNPAGETWYIOSLCSLRRCPRGDDILITILEVNEYVSN 452
QY 246 EFESFSDATFHAKKQIPCTIVSMITKELYF 275
DB 453 K-----DDKKNMGKOMPQPTFTLRKKLYF 476

RESULT 14
US-09-952-768-4

Sequence 4, Application US/09952768
Patent No. US20020035242A1
GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE.

NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
us-09-952-768-4

Query Match 28.8%; Score 421; DB 10; Length 496;
Best Local Similarity 37.8%; Pred. No. 1.1e-33;
Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;

QY 24 SESMDSGISLDNSYKMDYEMGICITIIINKNFKHST-----GMSRSRGTDVDAANLRE 76
DB 234 SESQ-----TLDKYOMKSRPGCYCLIIINNHNFAKAREKVPKLSIRDRNGTHLDAGALLT 289
QY 77 TFRNLKYEVRNKNDLTREETVELMRDYSKEDHSKSSFCVLLSHGEGIIIFGTNG--PVD 135
DB 290 TFEELHFEIRPHDCTVEQIYEILKIYOLMDHSMDCFCIIISHGDKGIITGDOGEAP 349
QY 136 LKKTINFEPRDRSLTGKPKLFIIOACRGTELDGCI--ETDSC-----VDDMACHK--- 186
DB 350 IYELTSQFTGLKCPSLAGKPKVFFIOACQGDNYOKGIPVETDSEOPYLEMDLSSPQTRY 409
QY 187 IPEADFLVAYSTAPGYYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNRKVAT 245
DB 410 IPDEADFLGMATVNNCVSRNPAGETWYIOSLCSLRRCPRGDDILITILEVNEYVSN 469
QY 246 EFESFSDATFHAKKQIPCTIVSMITKELYF 275
DB 470 K-----DDKKNMGKOMPQPTFTLRKKLYF 493

RESULT 15
US-10-068-569-1

Sequence 1, Application US/10068569
Patent No. US20020160975A1
GENERAL INFORMATION:

APPLICANT: Stiniyasa, Stiniyasa M.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin

TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1
LENGTH: 416
TYPE: PRT
ORGANISM: Homo sapiens
us-10-068-569-1

Query Match 28.5%; Score 417; DB 9; Length 416;
Best Local Similarity 33.2%; Pred. No. 2.1e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 34 DNSYKMDYEMGICITIIINKNFKHSTGMSRSRGTDVDAANLRETFRNLYEVRNKNDLTR 93
DB 150 DLAITLSMEPCGHCLIIINNHNFAKAREKVPKLSIRDRNGTHLDAGALLT 209
QY 94 EIVELMRDYSKEDHSKSSFCVLLSHGEE-----GIIFGTNG--PVDLKTITNFFRG 145
DB 210 KKMVALLELAQODHGALDCCVAVILLSHGQASHLOFPAVAVGTGDCPVSEKIVNIFNG 269
QY 146 DRCRSLTGKPKLFIIOACRGTELDGCIETDSCVDDM----- 182
DB 270 TSCPSLGKPKLFIIOACRGTELDGCIETDSCVDDM----- 182
QY 183 -ACHRIPEADFLVAYSTAPGYYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNR 241
DB 330 DAISLPTPDSIDFVSYSTFPGVSRNDRKSSGMYVETLDDITFEQNAHSDLOSLLIRVAN 389
QY 242 KVATEFESFSDATFHAKKQIPCTIVSMITKELYF 275
DB 390 AVSVK-----GIYKMGKCPNPLRKKLYF 413

Search completed: December 2, 2002, 13:04:19
Job time : 8.64138 secs


```

FT Region 176..193
FT /note= "amino-terminal sequence determined for
FT Region 161..165 purified enzyme subunits"
FT /note= "conserved pentapeptide containing putative
FT Protein 176..277 catalytic cysteine"
FT /note= "12 kDa subunit p12"
PN MO9633268-A1.
XX
XX
PD 24-OCT-1996.
XX
XX
PF 17-APR-1996; 96MO-US05282.
XX
XX
PR 21-APR-1995; 95US-0426557.
XX
XX
PA (MER1 ) MERCK & CO INC.
XX (MER1 ) MERCK FROST CANADA INC.
XX
XX
PI All A, Miller DK, Nicholson DW, Thornberry NA, Vallancourt JP;
XX WPI; 1996-485775/48.
XX
XX
PS Claim 1; Fig 4C; 84pp; English.
XX
XX
CC The present sequence is the CPP23beta or Glu190 isoform of the
CC inactive CPP32 proenzyme (a member of the interleukin converting
CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of
CC unknown function cloned from Jurkat cells), the proteolytic product
CC of which is the poly(DP-ribose) polymerase (PARP) protease,
CC apopain. The PARP cleavage enzyme was purified from the human
CC monocytic leukemia cell line, THP-1, using standard ion exchange
CC chromatography techniques and SDS PAGE. Apopain can be used to
CC identify apopain activity modulators, while apopain encoding DNA
CC may be used for apopain production or in gene therapy (i.e. in vivo
CC or ex vivo gene transplantation) for enhancing the pro-inflammatory
CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and
CC antisense DNA can be used to reduce or eliminate the
CC pro-inflammatory or pro-apoptotic effects of apopain. Modulation
CC of apopain activity is beneficial in the treatment of immune,
CC disease, degenerative diseases, e.g. AIDS, autoimmune
CC disease, pathogenic infections, cardiovascular and neurological
CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
CC and Alzheimer's disease.
XX
XX
SO Sequence 277 AA:

```

Query Match 100.0%; Score 1463; DB 17; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1e-147;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 MENTENSVDKSIKMLEKIIHGSESDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Db 1 MENTENSVDKSIKMLEKIIHGSESDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Oy 61 MTSRSGTDVDAANLRETFRNKLYEVRNKNLDTREIVELMRVSKDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVRNKNLDTREIVELMRVSKDHSKRSSFVCVLLS 120
Oy 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Db 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Oy 181 DMACHKRIPEADFLIAYSTAGYYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Db 181 DMACHKRIPEADFLIAYSTAGYYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Oy 241 KRVATEFSFSDATFPAKKQIPCIIVSMLTKELYFYH 277

```

```

Db 241 KRVATEFSFSDATFPAKKQIPCIIVSMLTKELYFYH 277
RESULT 2
ID AAM00677 standard; Protein; 277 AA.
XX
XX
AC AAM00677;
XX
XX
DT 06-DEC-1996 (first entry)
XX
XX
DE Pro-Yama.
XX
XX
KM Yama; CrmA; apoptosis; Fas receptor; T-lymphocyte; AIDS; HIV;
KM human immunodeficiency virus.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9625501-A2.
XX
XX
PD 22-AUG-1996.
XX
XX
PF 09-FEB-1996; 96MO-US01882.
XX
XX
PR 01-JUN-1995; 95US-0457731.
XX 13-FEB-1995; 95US-0389812.
XX
XX
PA (UNMT ) UNIV MICHIGAN.
XX
XX
XX Dixit VM;
XX
XX
DR WPI; 1996-393402/39.
XX
XX
DR N-PSDB; AAT33567.
XX
XX
PT New nucleic acid encoding Yama protein or CrmA mutant - useful for
PT modulating apoptosis, maintaining T cell viability in AIDS patients
PT and for drug screening
XX
XX
PS Disclosure; Fig 1; 118pp; English.
XX
XX
CC Human pro-Yama (AAM00677) is a zymogen which upon activation cleaves
CC PARP to an 85 kDa form. Activated Yama has the ability to modulate
CC cellular function associated with the Fas receptor pathway such as
CC Fas-associated apoptosis. This activity is inhibited by CrmA (see
CC also AAM00678). The pro-Yama sequence was deduced from a cDNA clone
CC isolated from human umbilical vein endothelial cells. Yama can be
CC produced in a host cell and used to modulate cellular function, to
CC raise antibodies, or to screen for agents or drugs which modulate
CC a Fas-related function such as apoptosis.
XX
XX
SO Sequence 277 AA:

```

Query Match 100.0%; Score 1463; DB 17; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1e-147;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 MENTENSVDKSIKMLEKIIHGSESDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Db 1 MENTENSVDKSIKMLEKIIHGSESDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Oy 61 MTSRSGTDVDAANLRETFRNKLYEVRNKNLDTREIVELMRVSKDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVRNKNLDTREIVELMRVSKDHSKRSSFVCVLLS 120
Oy 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Db 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Oy 181 DMACHKRIPEADFLIAYSTAGYYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Db 181 DMACHKRIPEADFLIAYSTAGYYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240

```

OY 241 RKVATEFESFDPATFHAKKOIPCIYVSMLEKELYFH 277
DB 241 RKVATEFESFDPATFHAKKOIPCIYVSMLEKELYFH 277

RESULT 3
AAR5831
ID AAR5831 standard; Protein; 277 AA.

AC AAR5831;
DT 28-OCT-1996 (first entry)

DE Human interleukin-1-converting enzyme-like apoptosis protease-4.
XX ICB-LAP-4; interleukin-1-converting enzyme-like apoptosis protease;
XX enzyme; Alzheimer's disease; Parkinson's disease; septic shock;
XX head injury; rheumatoid arthritis.

OS Homo sapiens.

PN W09613603-A1.

PD 09-MAY-1996.

PF 06-JUN-1995; 95WO-US07235.

PR 01-NOV-1994; 94US-0334251.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Hastings GA, He W, Hudson PL, Rosen CA;

DR WPI; 1996-239509/24.

DR N-PSDB; AAT15277.

PT Human ICB-LAP-3 and -4 DNA and protein - useful in the diagnosis
PT and treatment of Alzheimer's disease, Parkinson's disease,
PT rheumatoid arthritis, septic shock and head injury

PS Claim 1: Page 44; 67pp; English.

CC This ICB-LAP-4 protein may be used therapeutically, e.g. as an
CC antitumor or antiviral agent and to control embryonic development
CC and tissue homeostasis. The protein can also be used to treat
CC immunosuppression disorders, such as AIDS, by targeting virus
CC infected cells for cell death. The DNA may find use in gene
CC therapy applications.

SO Sequence 277 AA:

Query Match 100.0%; Score 1463; DB 17; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MENTENSVDKSKIKNLEPKIIGHSESDSGISLDNSYKMDYPMGLCIITINKNFHSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIGHSESDSGISLDNSYKMDYPMGLCIITINKNFHSTG 60

OY 61 MTSRSGTDVDAANLRETFNKLKYEVRANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120
DB 61 MTSRSGTDVDAANLRETFNKLKYEVRANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120

OY 121 HGEEGIIIFGTNGPVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVDD 180
DB 121 HGEEGIIIFGTNGPVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVDD 180

OY 181 DMACHRIPEADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240
DB 181 DMACHRIPEADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240

OY 241 RKVATEFESFDPATFHAKKOIPCIYVSMLEKELYFH 277
DB 241 RKVATEFESFDPATFHAKKOIPCIYVSMLEKELYFH 277

DB 241 RKVATEFESFDPATFHAKKOIPCIYVSMLEKELYFH 277

RESULT 4
AAM41688
ID AAM41688 standard; Protein; 277 AA.

AC AAM41688;
DT 02-JUL-1998 (first entry)

DE Amino acid sequence of a protein designated YAMA.

XX CrmA; tumour necrosis factor receptor; TNF-R; U1-70; inhibition;
XX apoptosis; activation; U1-70 path; apoptosis path; identification;
XX modulation.

OS Synthetic.

PN JP09299077-A.

PD 25-NOV-1997.

PF 27-JAN-1997; 97JP-0012932.

PR 09-FEB-1996; 96US-0591605.

PA (UNMI) UNIV MICHIGAN.

DR WPI; 1996-056551/06.

DR N-PSDB; AAV05471.

PT Controlling apoptosis by inhibiting activation of the U1-70 pathway
PT - by introduction of nucleic acid encoding protein with CrmA
PT biological activity into the cell

PS Disclosure; Fig 2; 48pp; Japanese.

CC The present sequence represents a non-naturally occurring protein
CC designated YAMA. The specification describes a novel method of
CC controlling cell functions controlled by the tumour necrosis factor
CC receptor (TNF-R) pathway containing U1-70. The method comprises
CC introducing a nucleic acid molecule encoding CrmA into a cell, and
CC culturing the cell under suitable conditions for transcription and
CC translation of the CrmA nucleic acid. Method for preventing and
CC inhibiting apoptosis by inhibiting activation of the U1-70 path,
CC identifying the chemical related to the apoptosis path, and screening a
CC candidate chemical having biological function in the apoptosis path are
CC also described. The methods can be used to identify substances which
CC modulate apoptosis in cells controlled by the TNF-R pathway.

SO Sequence 277 AA:

Query Match 100.0%; Score 1463; DB 19; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MENTENSVDKSKIKNLEPKIIGHSESDSGISLDNSYKMDYPMGLCIITINKNFHSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIGHSESDSGISLDNSYKMDYPMGLCIITINKNFHSTG 60

OY 61 MTSRSGTDVDAANLRETFNKLKYEVRANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120
DB 61 MTSRSGTDVDAANLRETFNKLKYEVRANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120

OY 121 HGEEGIIIFGTNGPVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVDD 180
DB 121 HGEEGIIIFGTNGPVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVDD 180

OY 181 DMACHRIPEADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240
DB 181 DMACHRIPEADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240

QY 241 RKVATFESEFSDATFHAKKQIPICIYMLTKELYFH 277
 DB 241 RKVATFESEFSDATFHAKKQIPICIYMLTKELYFH 277
 RESULT 5
 AAM16600
 ID AAM16600 standard; protein; 277 AA.
 XX
 AC AAM16600;
 XX
 DT 26-JUN-1997 (first entry)
 XX
 DE Apoptain CPP32a proenzyme.
 XX
 KM CPP32a; isoform; inactive; CPP32; proenzyme; cysteine; protease;
 KM proteolytic product; poly(DP-ribose) polymerase; PARP; apoptain;
 KM cleavage enzyme; human; monocytic leukemia; cell line; THP-1;
 KM identification; modulator; recombinant production; gene therapy;
 KM pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody;
 KM antisense DNA; treatment; immune; proliferation; degeneration;
 KM disease; AIDS; acquired immunodeficiency syndrome; autoimmune;
 KM pathogenic infection; cardiovascular; neurological; injury;
 KM alopecia; ageing; cancer; type I diabetes; Parkinson's;
 KM Alzheimer's.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Location/Qualifiers
 FT 1..28
 FT /note= "amino-terminal pro-domain"
 FT 28..29
 FT Region
 FT 29..46
 FT /note= "amino-terminal sequence determined for
 FT purified enzyme subunits"
 FT 29..175
 FT /note= "17 kDa subunit p17"
 FT 175..176
 FT Region
 FT 176..193
 FT /note= "amino-terminal sequence determined for
 FT purified enzyme subunits"
 FT 161..165
 FT /note= "conserved pentapeptide containing putative
 FT catalytic cysteine"
 FT 176..277
 FT /note= "12 kDa subunit p12"
 XX
 PN WO9633268-A1.
 XX
 PD 24-OCT-1996.
 XX
 PF 17-APR-1996; 96WO-US05282.
 XX
 PR 21-APR-1995; 95US-0426557.
 XX
 PA (MERI) MERCK & CO INC.
 PA (MERI) MERCK FROST CANADA INC.
 XX
 P1 All A, Miller DK, Nicholson DW, Thornberry NA, Vaillancourt JP;
 XX
 DR WPI; 1996-485775/48.
 XX
 FT Apoptain, a new human apoptosis related enzyme - responsible for the
 FT proteolytic breakdown of poly(ADP- ribose) polymerase (PARP) which
 FT occurs at the onset of apoptosis
 XX
 PS Claim 1; Page -: 84pp; English.
 XX
 CC The present sequence is the CPP32a or Asp190 isoform of the
 CC inactive CPP32 proenzyme (a member of the interleukin converting
 CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of
 CC unknown function cloned from Jurkat cells), the proteolytic product
 CC of which is the poly(DP-ribose) polymerase (PARP) protease,

CC apoptain. The PARP cleavage enzyme was purified from the human
 CC monocytic leukemia cell line, THP-1, using standard ion exchange
 CC chromatography techniques and SDS PAGE. Apoptain can be used to
 CC identify apoptain activity modulators, while apoptain encoding DNA
 CC may be used for apoptain production or in gene therapy (i.e. in vivo
 CC or ex vivo gene transplantation) for enhancing the pro-inflammatory
 CC or pro-apoptotic effects of apoptain. Anti-apoptain antibodies and
 CC antisense DNA can be used to reduce or eliminate the
 CC pro-inflammatory or pro-apoptotic effects of apoptain. Modulation
 CC of apoptain activity is beneficial in the treatment of immune,
 CC proliferative and degenerative diseases, e.g. AIDS, autoimmune
 CC disease, pathogenic infections, cardiovascular and neurological
 CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
 CC and Alzheimer's disease.
 XX
 SQ Sequence 277 AA;
 XX
 Query Match 99.8%; Score 1460; DB 17; Length 277;
 Best Local Similarity 99.6%; Pred. No. 2.2e-147;
 Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MENTENSVDKSKIKNLEPKIHGSESDSGISLDSYKMDYPEMGICIIINNKHFHSTG 60
 DB 1 MENTENSVDKSKIKNLEPKIHGSESDSGISLDSYKMDYPEMGICIIINNKHFHSTG 60
 QY 61 MTSRSGTDVDAANLRETFRNKATEVRNKNKNDLTREBEIVELMRDYSKEDHSKRSSFVCLLS 120
 DB 61 MTSRSGTDVDAANLRETFRNKATEVRNKNKNDLTREBEIVELMRDYSKEDHSKRSSFVCLLS 120
 QY 121 HGEGLIIFGTNGPVDLKITTFNFRGDRCSLTGPKLFIIOACRGTELDGIEFDSGVDD 180
 DB 121 HGEGLIIFGTNGPVDLKITTFNFRGDRCSLTGPKLFIIOACRGTELDGIEFDSGVDD 180
 QY 181 DMACHKIPVEADFLVASTAPGYYSWRNSKDSGSMFTQSICAMLKQYADKLEFPHILTRVN 240
 DB 181 DMACHKIPVEADFLVASTAPGYYSWRNSKDSGSMFTQSICAMLKQYADKLEFPHILTRVN 240
 QY 241 RKVATFESEFSDATFHAKKQIPICIYMLTKELYFH 277
 DB 241 RKVATFESEFSDATFHAKKQIPICIYMLTKELYFH 277
 RESULT 6
 AAY21717
 ID AAY21717 standard; Protein; 277 AA.
 XX
 AC AAY21717;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of caspase-3 (CPP32).
 XX
 KM Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 KM autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 KM tumour cell; myocardial infarction; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9935277-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 11-JAN-1999; 99WO-US00632.
 XX
 PR 09-JAN-1998; 98US-0070987.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemrl ES;
 XX
 DR WPI; 1999-419353/35.
 DR N-FSDB; AAX81219.
 XX

PT New isolated nucleic acid molecule encoding a rev-caspase - used
 PT for screening and identifying inhibitors or enhancers for treating
 PT cancer or autoimmune disease

PS Disclosure; Fig 13A-B; 74pp; English.

CC The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumor cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AA081217-AA081226 represent human caspase genes encoding caspase 1-10
 CC gene products (AA021715-Y21724).

XX Sequence 277 AA;

Query Match 99.8%; Score 1460; DB 20; Length 277;

Best Local Similarity 99.6%; Pred. No. 2.2e-147;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKINLEPKITIHGSESDSGISLDSYKMDYPMGLCTIINKNFKHSTG 60

DB 1 MENTENSVDKSKINLEPKITIHGSESDSGISLDSYKMDYPMGLCTIINKNFKHSTG 60

QY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120

DB 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120

QY 121 HGEEGITFGNGPVDLKKTINFFRGDRCSLTGKPKLFTIOACRGTELDGCIETDGVDD 180

DB 121 HGEEGITFGNGPVDLKKTINFFRGDRCSLTGKPKLFTIOACRGTELDGCIETDGVDD 180

QY 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240

DB 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240

QY 241 RKVATEFESFSDATFPAKKOIPCIVSMLTKELEYFH 277

DB 241 RKVATEFESFSDATFPAKKOIPCIVSMLTKELEYFH 277

RESULT 7
 AA005394
 ID AA005394 standard; Protein; 277 AA.

XX AA005394;

AC AA005394;

DT 24-OCT-2001 (first entry)

XX Human caspase 3.

XX Human; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;

KW viral infection; haematopoietic disorder; autoimmune disorder;

KW atherosclerosis; neurological disorder.

XX Homo sapiens.

XX WO200153310-A1.

XX 26-JUL-2001.

PF 11-JAN-2001; 2001MO-US00888.

PR 18-JAN-2000; 2000US-0484617.

PA (ISIS-) ISIS PHARM INC.

XX Zhang H, Cowser LM;

XX WPI: 2001-442252/47.

DR N-PSDB: AAS10503.

XX New antisense compound to inhibit caspase 3 is useful for treating

PT hepatitis and atherosclerosis -

PS Disclosure; Page 92-94; 127pp; English.

CC The present sequence representing human caspase 3 is described
 CC in an invention relating to novel antisense oligonucleotides
 CC (AAS10517-AAS10676) and methods of using these compounds for the
 CC modulation of caspase 3 expression. The caspase 3 antisense
 CC oligonucleotides specifically hybridise with and inhibit the
 CC expression of caspase 3. Antisense compounds targeted to caspase 3
 CC are useful to inhibit caspase 3 expression in cells or tissues and
 CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are
 CC useful for treating disorders associated with expression of caspase 3.
 CC Such disorders include hyperproliferative disorders (e.g. cancer),
 CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune
 CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
 CC disease).

XX Sequence 277 AA;

Query Match 99.8%; Score 1460; DB 22; Length 277;

Best Local Similarity 99.6%; Pred. No. 2.2e-147;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKMLPEKITHGSESDSGISLDSYKMDYPMGLCTIINKNFKHSTG 60

DB 1 MENTENSVDKSKIKMLPEKITHGSESDSGISLDSYKMDYPMGLCTIINKNFKHSTG 60

QY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120

DB 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120

QY 121 HGEEGITFGNGPVDLKKTINFFRGDRCSLTGKPKLFTIOACRGTELDGCIETDGVDD 180

DB 121 HGEEGITFGNGPVDLKKTINFFRGDRCSLTGKPKLFTIOACRGTELDGCIETDGVDD 180

QY 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240

DB 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240

QY 241 RKVATEFESFSDATFPAKKOIPCIVSMLTKELEYFH 277

DB 241 RKVATEFESFSDATFPAKKOIPCIVSMLTKELEYFH 277

RESULT 8
 AA006000
 ID AA006000 standard; Protein; 277 AA.

XX AA006000;

AC AA006000;

DT 02-JUL-2001 (first entry)

XX Human caspase-3.

XX Human; caspase-3; CPP32; yama; apopain;

KW cysteine protease; apoptosis; caspase expression cassette; metastasis;

KW tumour; cathepsin B; urokinase; proliferation; gene therapy.

XX Homo sapiens.

XX Key

FT Cleavage-site 9..10 Location/Qualifiers

FT Cleavage-site 28..29 /Label= Proteolytic_cleavage_site

The present amino acid sequence is human Caspase-3 also known as CPP32, yama and apopain. Caspases are a family of cysteine proteases, that participate in the initiation and execution of apoptosis. Caspases exist as pro-enzymes, activated by cleavage into a large and small subunit, occurring after specific aspartic acid residues within the pro-enzyme sequence. The present invention relates to a method for functional cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage site not associated in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA encoding fusion polypeptide is used in gene therapy.

RESULT 9

RESULT 10	
AAW48945	
ID AAW48945	standard; protein; 277 AA.
XX	

PT treating Alzheimer's disease, amyotrophic lateral sclerosis, and
 PT other neurodegenerative disorders
 PS Claim 1; Page 65; 76pp; English.
 XX
 CC This polypeptide comprises a novel rat interleukin-1 beta
 CC converting enzyme (ICE) related protease, overexpression of which
 CC may be involved in a neuronal death cascade. The amino acid
 CC sequence was deduced from a cDNA clone (see AAV1959) isolated from a
 CC rat brain cDNA library. ICE related protease is present in the
 CC central nervous system and is enriched in central neurons
 CC including pyramidal neurons and granule neurons of the hippocampus
 CC and cerebral cortex. An expression vector capable of producing the
 CC ICE related protease in a host cell is claimed. The protease can
 CC be used in a claimed method to identify compounds that inhibit
 CC apoptosis. Such inhibitors can be used to treat Alzheimer's
 CC disease, amyotrophic lateral sclerosis (ALS), head trauma or other
 CC neurodegenerative disorders in humans (all claimed). Antibodies
 CC raised against the protease may be used for diagnosis of these
 CC disease states, or in their treatment.
 SO Sequence 277 AA;
 XX
 Query Match 89.1%; Score 1304; DB 19; Length 277;
 Best Local Similarity 88.4%; Pred. No. 1e-130;
 Matches 245; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MENTENSVDKSKIKNLEPKIIHGSEMDGSLDINSYKMDYEMGLCIIINKNFHKSTG 60
 DB 1 MONTNRSVDSKSIINPEKTIHSGSKSDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60
 QY 61 MTSRSGTVDVDAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120
 DB 61 MSRRNSTDVDAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120
 QY 121 HGEBSGIIFGTNGPVDLKKTINFFRGDCRSLTGKPKLFIIOACRGTELDGCIETDGSVD 180
 DB 121 HGEBSGIIFGTNGPVDLKKTINFFRGDCRSLTGKPKLFIIOACRGTELDGCIETDGSVD 180
 QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIOSLCAALKOYADKLEFMHILTRVN 240
 DB 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIOSLCAALKOYADKLEFMHILTRVN 240
 QY 241 RRVATEFESFSDATFHAKKOIPCIVSMLTRELYFYH 277
 DB 241 RRVATEFESFSDATFHAKKOIPCIVSMLTRELYFYH 277
 XX
 RESULT 14
 AAG78712
 ID AAG78712 standard; Protein; 277 AA.
 XX
 AC AAG78712;
 XX
 DT 11-DEC-2001 (first entry)
 XX
 DE Pig caspase #2.
 XX
 KW Pig; caspase; inflammation; infection.
 XX
 OS Sus scrofa.
 XX
 PN JP2001169785-A.
 XX
 PD 26-JUN-2001.
 XX
 PE 03-OCT-2000; 2000JP-0303931.
 XX
 PR 05-OCT-1999; 99JP-0284829.
 XX
 PA (NORO) NORINSUISANSHO KACHIKU EISEI.
 PA (MUNE) MUNEY Y.
 PA (MORI) MORI Y.

PA (SHIM) SHIMOCHI Y.
 PA (ARAI) ARAI K.
 XX
 DR WPI; 2001-592539/67.
 DR N-PSDB; AAI66510.
 XX
 PT Structural gene of swine caspase family, used for artificial control of
 PT inflammatory reactions in infectious diseases
 PS Claim 6; Page 16; 23pp; Japanese.
 XX
 CC The present invention provides two versions of a porcine caspase protein.
 CC These can be used to control inflammatory reactions to microbial or viral
 CC infectious diseases. The present sequence is one version of the protein
 CC of the invention.
 CC
 SO Sequence 277 AA;
 XX
 Query Match 88.6%; Score 1296; DB 22; Length 277;
 Best Local Similarity 88.4%; Pred. No. 7.5e-130;
 Matches 245; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MENTENSVDKSKIKNLEPKIIHGSEMDGSLDINSYKMDYEMGLCIIINKNFHKSTG 60
 DB 1 MENTNSVDSKSIKLEPKIIHGSKSDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60
 QY 61 MTSRSGTVDVDAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120
 DB 61 MACSSGTVDVDAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120
 QY 121 HGEBSGIIFGTNGPVDLKKTINFFRGDCRSLTGKPKLFIIOACRGTELDGCIETDGSVD 180
 DB 121 HGEBSGIIFGTNGPVDLKKTINFFRGDCRSLTGKPKLFIIOACRGTELDGCIETDGSVD 180
 QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIOSLCAALKOYADKLEFMHILTRVN 240
 DB 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIOSLCAALKOYADKLEFMHILTRVN 240
 QY 241 RRVATEFESFSDATFHAKKOIPCIVSMLTRELYFYH 277
 DB 241 RRVATEFESFSDATFHAKKOIPCIVSMLTRELYFYH 277
 XX
 RESULT 15
 AAU05395
 ID AAU05395 standard; Protein; 277 AA.
 XX
 AC AAU05395;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Mouse caspase 3.
 XX
 KW Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;
 KW viral infection; haematopoietic disorder; autoimmune disorder;
 KW atherosclerosis; neurological disorder.
 XX
 OS Mus musculus.
 XX
 PN WO200153310-A1.
 XX
 PD 26-JUL-2001.
 XX
 PE 11-JAN-2001; 2001WO-US00888.
 XX
 PR 18-JAN-2000; 2000US-0484617.
 XX
 PA (ISIS-) ISIS PHARM INC.
 PA Zhang H, Cowsett LM;
 PI
 XX WPI; 2001-442252/47.
 DR N-PSDB; AAS10510.

XX New antisense compound to inhibit caspase 3 is useful for treating
PT hepatitis and atherosclerosis -
XX
PS Disclosure; Page 96-97; 127pp; English.
XX

CC The present sequence representing mouse caspase 3 is described
CC in an invention relating to novel antisense oligonucleotides
CC (AS10517-AS10676) and methods of using these compounds for the
CC modulation of caspase 3 expression. The caspase 3 antisense
CC oligonucleotides specifically hybridise with and inhibit the
CC expression of caspase 3. Antisense compounds targeted to caspase 3
CC are useful to inhibit caspase 3 expression in cells or tissues and
CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are
CC useful for treating disorders associated with expression of caspase 3.
CC Such disorders include hyperproliferative disorders (e.g. cancer),
CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune
CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
CC disease).
XX

SQ Sequence 277 AA:

Query Match 88.4%; Score 1293; DB 22; Length 277;
Best Local Similarity 86.6%; Pred. No. 1.6e-129;
Matches 240; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

OY 1 MENTENSVDKSIKNEPKIHGSESDSGISLDNSGYKMDYPMGICITINNKPFHKS 60
DB 1 MENTENSVDKSIKNEPKIHGSESDSGISLDNSGYKMDYPMGICITINNKPFHKS 60
OY 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIYELMDVSKEDHSKSSFCVLLS 120
DB 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIYELMDVSKEDHSKSSFCVLLS 120
OY 121 HGEELIIGTNGPVDLKRTTNFRGDRCSLTGKPKFTIIOACRGTELDGIGTDSGVD 180
DB 121 HGEELIIGTNGPVDLKRTTNFRGDRCSLTGKPKFTIIOACRGTELDGIGTDSGVD 180
OY 181 DMACHKIPVADFLYAVSTAPGYYSWRNSKDSWFTOSLCAMLKOYADKLEFPHILTRVN 240
DB 181 DMACHKIPVADFLYAVSTAPGYYSWRNSKDSWFTOSLCAMLKOYADKLEFPHILTRVN 240
OY 241 RRVATEFESFSDATFHAHKKQIPCIIVSMLTKELYFYH 277
DB 241 RRVATEFESFSDATFHAHKKQIPCIIVSMLTKELYFYH 277

Search completed: December 2, 2002, 12:56:04
Job time : 32.0431 secs

100

05 Mus musculus (Mouse).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

05 Mus musculus (Mouse).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RT Fortin J.-P., Sekaly R.-P.;
RL "Multiple Pathways of Apoptosis Converging on the CPP32 Protease.";
EMBL: U63720; AAD09504.1; -
DR HSSP: P42574; IPAU.
DR MEROPS: C14.003; -
DR MGD: MGI:107739; Casp3.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBCEZYME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KM Protease.
FT NON_TER
SQ SEQUENCE 220 AA; 25050 MW; FE7F4857C4EBA544 CRC64;

Query Match 71.18; Score 1040; DB 11; Length 220;
Best Local Similarity 86.8%; Pred. No. 2.9e-79;
Matches 191; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 58 STMTSGSTGVDAANLRETFRNLYEVNKNNDLTREIYVLMRDVSKEDHSKRSFVCV 117
DB 1 STGMSANGNDVDAANLRETFRNLYEVNKNNDLTREIYVLMRDVSKEDHSKRSFVCV 60
QY 118 LLSHGEGLIFGTNGPVDLKLTNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSG 177
DB 61 ILSHGDEGVLYGTNGPVDELKLTSEFRGDCRSLTGKPKLFTIOACRGTELDGCIETDSG 120
QY 178 VDDDMACHTPVEADFLYATSTAPGYISWRNSKDGSWFIOSLCAMLYADKLEFMHILT 237
DB 121 TDEMACQKTPVEADFLYATSTAPGYISWRNSKDGSWFIOSLCAMLYADKLEFMHILT 180
QY 238 RVNRKVATEFESFSDATFPAKKQIPCIYVSMLTKELYFYH 277
DB 181 RVNRKVATEFESFSDATFPAKKQIPCIYVSMLTKELYFYH 220

RESULT 5
093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.L., Bridgman J.T.;
RL "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells.";
EMBL: AF083029; AAC32602.1; -
DR HSSP: P42574; IPAU.
DR MEROPS: C14.003; -
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
SQ SEQUENCE 182 AA; 20408 MW; B5860CC6596C21BE7 CRC64;
```

```
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBCEZYME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 65.5%; Score 958; DB 13; Length 283;
Best Local Similarity 66.4%; Pred. No. 2.9e-72;
Matches 180; Conservative 43; Mismatches 46; Indels 2; Gaps 2;

QY 5 ENSVDSKSIKNLEPKRIHGSSESDSGISLDNSKYMDPEMGLCTIINNNKFNKSTGMTSR 64
DB 13 EDVSDARSFPGSGMNLPAKSKVSDGILPDDSYRDYDEIGVCYIINNNKFNFRDGLSSR 72
QY 65 SGTVDANLNETFNLKLYEVNKNNDLTREIYVLMRDVSKEDHSKRSFVCVLLSHGEE 124
DB 73 SGTADAAVREVEPKLGYKVLNNDLSRDLFKLKNVSEEDHSKRSFVCVLLSHGDE 132
QY 125 GIIFGTNGPVDLKLTNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSGVDPMAC 184
DB 133 GLFYGTDGPLELKYVLSLFRGDKCSLTGKPKLFTIOACRGTELDGCIETDSG-PEYVC 191
QY 185 HKIPEADFLYATSTAPGYISWRNSKDGSWFIOSLCAMLYADKLEFMHILT RVNRKVA 244
DB 192 QKIPVEADFLYATSTAPGYISWRNSKDGSWFIOSLCAMLYADKLEFMHILT RVNRKVA 251
QY 245 TEFESFSDATFPAKKQIPCIYVSMLTKELYFYH 275
DB 252 -EYESCSTRDQFNNAKQIPCIYVSMLTKELYFYH 281

RESULT 6
077623 PRELIMINARY; PRT; 182 AA.
AC 077623;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-3 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.;
RT "Accumulation of Caspase-3 mRNA and Induction of Caspase Activity in
RT the Ovine Corpus Luteum Following Prostaglandin-P2a Treatment in
RT Vivo.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
EMBL: AF068837; AAC25713.1; -
DR HSSP: P42574; IPAU.
DR MEROPS: C14.003; -
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBCEZYME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
FT NON_TER
SQ SEQUENCE 182 AA; 20408 MW; B5860CC6596C21BE7 CRC64;

Query Match 58.4%; Score 854; DB 6; Length 182;
```


Best Local Similarity 87.48; Pred. No. 8.2e-64;
Matches 159; Conservative 12; Mismatches 11; Indels 0; Gaps 0.

QY	32	SLDNNYKMDYPMGCGIITINKNFKSTGWTSRSTDVDAANLRETFENLKYEVWRNKNDL	91
Db	1	SLEEBYKMDYPMGCGIITINKNFKSTGWTSRSTDVDAANLRETFENLKYEVWRNKNDL	60
QY	92	TREIIEVLMDYKSKEDHSKRSFPYVLLSHGEGIIETGNPVDLKTITNFRDRCRL	15
Db	61	TRKEMLELMDYKSKEDHSKRSFICVLLSHGEGIIETGNPVDLKTITNFRDRCRL	120
QY	152	TGKPLFLITQACRGTELDGCIETDPSGVDDDACHKIPEADFLVAYSTAPYYSWRNSKD	211
Db	121	TGKPLFLITQACRGTELDGCIETDPSGVDDDACHKIPEADFLVAYSTAPYYSWRNSKD	180
QY	212	GS 213	
Db	181	GS 182	

RESULT 7

ID	PRELIMINARY:	PRT:	282 AA.
AC	038U18		
AD	098U18		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Caspase-3.		
GN	CASP3.		
OS	Brachydanio rerio (zebrafish) (zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	Yabu T., Okazaki T., Yamashita M.;		
RT	"Molecular Cloning and Gene Expression of Zebrafish Caspase Related to		
RT	Mammalian Caspase-3."		
RL	Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.		
RL	EMBL: AB047003; BAB32409.1; -		
DR	HSSP: P42574; 1PAU.		
DR	MEROBS: C14_003; -.		
DR	ZEIN: ZDB-GENE-011210-1; casp3.		
DR	InterPro: IPR002398; ICE.		
DR	InterPro: IPR002138; ICE_p10.		
DR	InterPro: IPR001309; ICE_p20.		
DR	pfam: PR00655; ICE_p10; 1.		
DR	pfam: PR00656; ICE_p20; 1.		
DR	PRINTS: PR00376; ILIBCENZME.		
DR	SMART: SM00115; CASC. 1.		
DR	PROSITE: PS01122; CASPASE_HIS. 1.		
DR	PROSITE: PS01121; CASPASE_HIS. UNKNOWN_1.		
DR	PROSITE: PS50207; CASPASE_p10; 1.		
DR	PROSITE: PS50208; CASPASE_p20; 1.		
SO	SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;		

Query Match	53.5%	Score 782;	DB 13;	Length 282;
Best Local Similarity	61.8%;	Pred. No. 1.5e-57;		
Matches 146				

[illegible]

OY	215	FLOSICAMLOKOADLEEMHITVRNKNVATEEFESFSDATFAKKKOIPICVSMULTELY	274
		: : : : :	
Db	220	FLOSICEMWTKGSELELLOIMTRNRHVALLDEFTSINMPEFDKKOIPCIVSMULTREMY	279
OY	275	F 275	
Db	280	F 280	

RESULT 8

ID	PRELIMINARY:	PRT:	318 AA.
AC	091B65;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Caspase-7.		
GN	XCASPASE-7.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_Taxid=8355;		
RP	[1]		
RP	SEQUENCE FROM N. A.		
RX	MEDLINE=20209426; PubMed=10744739.		
RA	Nakajima K., Takahashi A., Yaota Y.;		
RT	Structure, expression and function of the Xenopus laevis caspase		
RT	family.;		
RL	J. Biol. Chem. 275:10484-10491(2000).		
DR	EMBL: AB038170; BAA94748.1; -.		
DR	HSSP: P42574; 1PAU.		
DR	MEROPS: C14.004; -.		
DR	InterPro: IPR002398; ICB.		
DR	InterPro: IPR002138; ICE_p10.		
DR	InterPro: IPR001309; ICE_p20.		
DR	Pfam: PF00655; ICE_p10; 1.		
DR	Pfam: PF00656; ICE_p20; 1.		
DR	PRINTS: PR00376; ILICBENZYM.		
DR	SMART: SM00115; CASC. 1.		
DR	PROSITE: PS01122; CASPASE_CYS. 1.		
DR	PROSITE: PS01121; CASPASE_HIS; UNKNOWN_1..		
DR	PROSITE: PS50207; CASPASE_P10. 1.		
DR	PROSITE: PS50208; CASPASE_P20. 1.		
Q	SEQUENCE 318 AA; 35337 MW; EBBC6684AF86A128 CRC64;		

Query Match	52.0%	Score 761	DB 13	Length 318
Best Local Similarity	52.4%	Pred. No. 1e-55		
Matches 153	Conservative 43	Mismatches 18	Gaps 4	

QY	2	ENHNSVDSIKNLEPKRIIHGSSM----	DSGISLDS-----	YKMDYPEMGICIT	49
		: : : : : : : : : : : : : : : : : : : :			
Db	24	EEGEDSVDAKPRDSQSRSTSSSTKKKKVEKDPKRTNNVAVIYPAFOYKMMNGVNGCIT			83
QY	50	INKNKPKSTGMTSRSGTVDAAANLRETFRNLYEVANKNDLTREELVEIEMRDVSKEDHS			109
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	84	INNKIEPKITGAMRNQTDIDARELLRCFGLGFVDVNVNKKSCOEEMENLLRTVAQDHK			143
QY	110	KRSFVCLLSHSEEGIIETGNGPVDAKKTITNEFRGRGCSLTKGPKRLFIIOACRGIELD			163
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	144	DSACFPACIFLSHSEEGIIETGDCAMPIKVLITLTERGNCNCSLGVKPKPLFTQACRGHEFD			203
QY	170	CGIETDSG--VDDMAC-----	NKIPVEADELYASTAPGYISWRNSKDSGSMFIQSILAML		223
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	204	DGLEADSGSVNDSLETDANDBRHKIPVEADELYASTVPGYISWRNPGMSGMFIQALCSVL			263
QY	224	KQYADLEFPHILITRYNRYKVAEEESGSPATPNAKQICPISYMLTKELF			275
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	264	NEGKLELVMOILITRYNLFVAIDFESYSDDPQSKKKQICPVASMLTKELF			315

RESULT 9
088550

```

ID 008550 PRELIMINARY; PRT; 303 AA.
AC 008550;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Forghani F., Roy S.;
RT "Rat Caspase-7 sequence."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072124; AAC24011.1;
DR HSSP; P42574; IPAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILBCENZTME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS0121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;

```

Query Match Best Local Similarity 50.9%; Score 745; DB 11; Length 303; Matches 153; Conservative 41; Mismatches 79; Indels 12; Gaps 3;

```

QY 3 NTESSVSVSKS-----INKLEPKIIHGSESDSGISLDN----SYKMDYPMNGLCIIINNK 53
DB 17 STEDGVDAKPRRSTIISSILWKKKKKNAKMCVSTTRDVPYLYLMDPEKKKCIINNK 76
QY 54 NFHKSTGMTSGSGTVDVAANRETFRNKLYEVRRKNDLTRREIYELAMDVSKEDSKSS 113
DB 77 NFEDATGMADVNRGTGDKDEALEFKCFRSGFEVYVYNDSCAKMODLLRRASEDSHNSAC 136
QY 114 FVCVLLSHGEGIIIFGTNGPVDLKKITNPFGRDRCRLTGPKLIIIOACGTEHDCIE 173
DB 137 FACVLLSHGEGNLLYGKDGVPYIKDLTAHFRGDKCKTILEPKLFFIIOACRTELDGIIQ 196
QY 174 TDSGVDDMAC--HKIPVEADFLYASTAGYYSWRNSKDSWFIQSICAMLKQYADKL 230
DB 197 ADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRNPKGSWVQALCSILNHGKDL 256
QY 231 EFMIILTRVNRKVAATEFESFDFATFAKKKQIPCVSKLTLELYP 275
DB 257 EIMQILTRVNDVARHFESQSDPRFNEKKQIPCVSKLTLELYP 301

```

RESULT 10

```

ID 099M47 PRELIMINARY; PRT; 276 AA.
AC 099M47;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase 6.
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

```

```

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002022; AAH02022.1; -.
DR HSSP; P42574; IPAU.
DR MGD; MGI:1312921; Casp6.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILBCENZTME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS0121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 276 AA; 31563 MW; 5965C5932A127B6C CRC64;

```

Query Match Best Local Similarity 36.0%; Score 526; DB 11; Length 276; Matches 104; Conservative 42; Mismatches 93; Indels 12; Gaps 1;

```

QY 37 YKMDYPMNGLCIIINNKNFHSTGMTSGTVDVAANRETFRNKLYEVRRKNDLTRREI 96
DB 20 YKMDHRRGVALIFNHERFWHLTLPERKGTNADRNLTFRSDLCFEVKKCFNDLAEEL 79
QY 97 VELARDVSKEDSKRRSSFEVCLLSHGEGIIIFGTNGPVDLKKITNPFGRDRCRLTGPKR 156
DB 80 LKIHIEVTSSTHIDADCFLCVFLSHGEGNHVYAYDAKIEIQTLTGFLKDGKCSLVGKKR 139
QY 157 LFIIQACRTELDGCIETDSGVD-----DDMACHKIPVEADFLYASTAGY 204
DB 140 IFIIQACRSGQHDVFPVPLDVVDHOTDKLDNTQYDVAASVYTLPAQADFLMCYSVAEGY 199
QY 205 SWRNSKDSGWFQSIQCAMLKQYADKLEFMHILTRVNRKVAATEFESFDFATFAKKQIQ 264
DB 200 SHRETVNSWYIQDLCEMLARAGSSLEFTELLTLVNRKVSQRVRVDCPKDPAIGKKQVPC 259
QY 265 IVSMLTKELYP 275
DB 260 FASMLTKLHF 270

```

RESULT 11

```

ID 09BOE7 PRELIMINARY; PRT; 293 AA.
AC 09BOE7;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Caspase 6; apoptosis-related cysteine protease.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004460; AAH04460.1; -.
DR EMBL; BC000305; AAH00305.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.005; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.

```

```

QY 2 ETWENV--DSKISKNLEFKIINGSSM-----DSGISLDP--NSKKADYEMGCII 49
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 KOTKSGLEKDNKNTSQTTF-----SENLEFETDGYFCSSSSTSMIPAETKYNNHKRGLALI 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 50 INKNFHKSTGMTSRSGTDVDAANLRETERFNLYEVRANKNDLIRELVELMARDVSKEDHS 109
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 FQOEHFEMHLRMPRPNGRTNADRNSLNKRFEDLNFEYQAFDNLKVEEVLQISOAAEANHA 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 KRSPFCVLLSHGEEIIIFGTNGPVDLKITNFRGDRCSLTGKRKPLFIQACRGTE-- 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 DADFCVCFVLSHGENDHVAAYDKTIAIDITALEFKGDKCSLVGKRIFFLQACRGDKHD 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 -----LDCCITDSGVDDMACIKRIYEADFLVATPAPCYWRNKSDDSWFIQSL 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 DVTFTMDVVDSEVKITNEVYVDAGVYITLTAGADFLICYSAEETYYSHRETIINSWTIQL 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 CAMEKQYADKLEFMHILTRVNRKVATEPESFSEDPATFHAKKOIPLCTIVSMILTKELF 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 CGAMKRFQDLSLEFTELLTLVNRKVSMSRYGNCNDKTAIGKKQVPCPSMULTRLYE 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
QY1B66 PRELIMINARY; PRT; 303 AA.
ID QY1B66
AC QY1B66;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-6.
GN XCASPASE-6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaota Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038169; BAA94747.1; -.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.005; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IILBCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 35.8%; Score 524; DB 13; Length 303;
Best Local Similarity 42.4%; Pred. No. 6,3e-36;
Matches 109; Conservative 48; Mismatches 86; Indels 14; Gaps
4,


```

Db 162 KSLVGRKPIFLIACRGEKHDEPLPKDEYDVELTNTVEYDASLC-TLPAGADFLMXY 220
 QY 198 STAPGYYSNMSNDGSGFIOSLCAMLKQYADKLEFMIILTRVNRKVAITEEFESFDPATFH 257
 Db 221 SVAEYYSNHEETVNGSVYIIDLCAVYKAVASLEFTEILTLVNRKVSORSVEYCNDRKAI 280
 QY 258 AKKOIPCIYSMLTKRELY 274
 Db 281 GKKOIPCFKSMITKLEF 297

RESULT 14

09D089

ID 09D089 PRELIMINARY: PRT: 276 AA.

AC 09D089: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE 10 days embryo cDNA, RIKEN full-length enriched library,
 clone:2610037G10, full insert sequence.

OS CASP6.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMBRYO;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann M., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schimi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RM EMBL: AK011710; BAB27792.1; -

DR HSSP: P42574; 1PAU.

DR MGD: MGI:1312921; Casp6.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002398; ICE.

DR Pfam: PF00655; ICE_p10; 1.

DR PRINTS: PR00376; ILBCEZYME.

DR SMART: SM00115; CASG. 1.

DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SQ SEQUENCE 276 AA; 31591 MW; 597EDF2321126B6C CRC64;

Query Match

Best Local Similarity 35.3%; Score 516; DB 11; Length 276;

Matches 103; Conservative 42; Mismatches 94; Indels 12; Gaps 1;

QY 37 YKMDYPMGICITINNNKFNKSTGTSRSGTDVDANLRETFNKLKYEVRNKNKDLTPEEI 96
 Db 20 YKMDHRRGVALIFNHRFFWHLTPERRGTNDRLTRRFSDLGFEVACFNDLRAEL 79

QY 97 VELNRDYSKEDHSKRSPFCVLLSHGEGIIFGTMGPVDLKITNPFGRDRLSLGKPK 156
 Db 80 LKLTIEHVSSTSHIDADDICVFLSHGEGNHYAYDAKLEIQTLPFGDKCOSLVGRPK 139
 QY 157 LFIIOACRGTLGDCIENFSDGVD-----DDMACHTIPVADFLYASTAPGY 204
 Db 140 IFTIIOACRGSHDVPVYFLDMVDHOTDKLDNVTQYDASVITLTPAGADFLMXYSAEGY 199
 QY 205 SWRNSKDGSWFIOSLCAMLKQYADKLEFMIILTRVNRKVAITEEFESFDPATFHAKQIPC 264
 Db 200 SHRETVNGSVYIIDLCEMLARYSGSLFEFTTEILTLVNRKVSORSVEYCNDRKAI 259
 QY 265 IVSMLTKRELY 275
 Db 260 FASMLTKLEF 270

RESULT 15

093415

ID 093415 PRELIMINARY: PRT: 304 AA.

AC 093415: 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE Caspase-6.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20149872; PubMed=10684799;

RA Johnson A.L., Bridgman J.T.;

RT "caspase-3 and -6 expression and enzyme activity in hen granulosa

RT cells.";

RL Biol. Reprod. 62:589-598(2000).

RM Pubmed=11953316;

DR HSSP: P42574; 1PAU.

DR MEROPS: C14.005; -

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002398; ICE.

DR Pfam: PF00655; ICE_p10; 1.

DR PRINTS: PR00376; ILBCEZYME.

DR SMART: SM00115; CASG. 1.

DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SQ SEQUENCE 304 AA; 34534 MW; 51CE31EBCAE7383 CRC64;

Query Match

Best Local Similarity 35.2%; Score 515; DB 13; Length 304;

Matches 102; Conservative 46; Mismatches 92; Indels 12; Gaps 1;

QY 37 YKMDYPMGICITINNNKFNKSTGTSRSGTDVDANLRETFNKLKYEVRNKNKDLTPEEI 96
 Db 49 YKMDHRRGVALIFNHRFFWHLTPERRGTNDRLTRRFSDLGFEVACFNDLRAEL 108
 QY 97 VELNRDYSKEDHSKRSPFCVLLSHGEGIIFGTMGPVDLKITNPFGRDRLSLGKPK 156
 Db 109 LKLTIEHVSSTSHIDADDICVFLSHGEGNHYAYDAKLEIQTLPFGDKCOSLVGRPK 168

Mon Dec 2 12:49:24 2002

us-09-895-263-4.rsp

Page 8

[illegible]

Search completed: December 2, 2002, 12:58:11
Job time : 27.2672 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 Search time 15.2828 Seconds

(without alignments)
1742.436 Million cell updates/sec

Title: US-09-895-263-4
Perfect score: 1463
Sequence: 1 MENTENSVDSKSKINLEPKI.....AKQIPCIIVSMLEKLYFYH 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_73:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1460	99.8	277	2	A55315
2	1308	89.4	277	2	S64710
3	1293	88.4	277	2	USC5410
4	996	68.1	212	2	I67437
5	437	29.9	454	2	JC7123
6	418	28.6	416	2	G02635
7	381.5	26.1	503	2	A49429
8	352	24.1	495	2	T20038
9	328.5	22.5	435	2	A54821
10	327.5	22.4	452	2	JC6507
11	310.5	21.2	536	2	T43633
12	306.5	21.0	826	2	T43638
13	277	18.9	642	2	T77021
14	274.5	18.8	242	2	JC7517
15	247.5	16.9	402	2	A46495
16	246.5	16.8	377	2	A57511
17	232.5	15.9	418	2	B57511
18	230.5	15.8	488	2	T13385
19	230	15.7	182	2	I67436
20	222.5	15.2	404	2	A52677
21	222	15.2	311	2	B56084
22	222	15.2	383	2	A56084
23	212	14.5	312	2	B54821
24	182	12.4	263	2	C56084
25	170.5	11.7	149	2	T43637
26	166	11.3	136	2	I53300
27	135.5	9.3	139	2	T43642
28	114.5	7.8	394	2	T26968
29	110	7.5	768	2	T18461

ALIGNMENTS

30	100.5	6.9	457	2	T05439	hypothetical prote
31	96	6.6	537	2	I51592	protein-tyrosine k
32	93	6.4	534	1	S33568	protein-tyrosine k
33	92.5	6.3	525	2	T31677	bactiracin synthet
34	91.5	6.3	642	2	D88951	protein C38C3.7 (1
35	91	6.2	629	2	AE2497	hypothetical prote
36	90.5	6.2	534	1	A44991	protein-tyrosine k
37	89	6.1	2052	2	C97038	phase-related prot
38	88	6.0	537	1	TVHUSY	protein-tyrosine k
39	88	6.0	600	2	S28496	microtubule-associ
40	88	6.0	781	2	C69452	signal-transducing
41	88	6.0	1087	2	T30330	gelatin-related p
42	87.5	6.0	299	2	D81384	probable lipoprote
43	87.5	6.0	552	2	S17551	gamma-aminobutyric
44	87.5	6.0	554	2	G01928	gamma-aminobutyric
45	87.5	6.0	556	2	S06838	gamma-aminobutyric

RESULT 1

A55315

Cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32

C:Species: Homo sapiens (man)

C>Date: 06-Feb-1995 #sequence, revision 06-Feb-1995 #text, change 01-Dec-2000

C:Accession: A55315; S58899; I39005

R:Fernandes-Alnemrl, T.; Iltwack, G.; Alnemrl, E.S.

J. Biol. Chem. 269, 30761-30764, 1994

A>Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans

A:Reference number: A55315; M01D:95074058; PMID:7983002

A:Accession: A55315

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-277 <PER>

A:Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666

R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant

; Yu, V.L.; Miller, D.K.

Nature 376, 37-43, 1995

A>Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammal

A:Reference number: S58899; M01D:95319529; PMID:7596430

A:Accession: S58899

A:Molecule type: protein

A:Residues: 29-46;176-189, 'E', 191-193 <NIC>

R:Newari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Polt

Cell 81, 801-809, 1995

A>Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable proteas

A:Reference number: A56924; M01D:95292347; PMID:7774019

A:Accession: I39005

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-189, 'E', 191-277 <RES>

A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match

Best local similarity 99.8%; Score 1460; DB 2; Length 277;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MENTENSVDSKSKINLEPKIIGHSEMDSGISLDNSYKMDYPMGLCTIINNKFNHSTG	60
DB	1	MENTENSVDSKSKINLEPKIIGHSEMDSGISLDNSYKMDYPMGLCTIINNKFNHSTG	60
QY	61	MNRSSTVDVDAANLRETFRNKLEVENKNDLTREELVELMRDVSKEHRSFVCYLLS	120
DB	61	MNRSSTVDVDAANLRETFRNKLEVENKNDLTREELVELMRDVSKEHRSFVCYLLS	120
QY	121	HEEEGIIFGTNGPVVDLKKITNFGRDRSLTKPKLFIIOACRGTELDGIFITDSGYDD	180
DB	121	HEEEGIIFGTNGPVVDLKKITNFGRDRSLTKPKLFIIOACRGTELDGIFITDSGYDD	180
QY	181	DMACHRIPEADFLYAVSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN	240

A: experimental source: embryo

R; Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T

[illegible]

RESULT 8
T20038
hypothetical protein C48D1.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20038
R:Burton, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19214
A:Accession: T20038
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-495 <WIL>
A:CROSS-references: EMBL:Z81049; PIDN:CAB02848.1; GSDSB:GN00022; CESP:C48D1.2
A:Experimental source: clone C48D1
C:Genetics:
A:Gene: CESP:C48D1.2
A:Map position: 4

A: Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 24.1%; Score 352; DB 2; Length 495;

Best Local Similarity 32.1%; Pred. No. 6.4e-21;

Matches 87; Conservative 43; Mismatches 95; Indels 46; Gaps 7;

2 ENTENSVDKSKIKNLEPKIHGSESDSGISLSDNSYKNDYFPMGLCTIINKNFKHSTGM 61

213 EEDMNFVDAPTLSR-----VFDEKTM-----YRNSSPRMCLITINNEHQ---M 255

62 TSGSTVDVAANLRETFRNLYEVNRKNDLTREIEVLMADVSKEDSKSSFEVCVLLSH 121

256 PIRNGKAKNDLNTNFRGCGYIVICKDNLTGKMLTITDFPAKHE-SHSDSALVLLSH 314

122 GEEGIIFTNG-PVDLKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSVD- 179

315 GEEVNIIGVDIPITSTHEIYDLNANAPRLAKPKITVFQACRGGERDNGFPLDSVDG 374

180 -----DDMAC-----HKIPVADFLYASTAPGYISMRNSKDG 213

375 VPAFLRGMDNRDGLNFENLGCVRPOVOQYMRKPPSOADILYATTAQYVSMNSARG 434

214 WFIOSLCAMLKOYADKLEFPHILTRVNRKVA 244

435 WFIOANCFVSTHAKMDVVELLETVNRKVA 465

RESULT 9

A: 4821

apoptosis regulator ICH-1, stimulatory form L - human

C: Species: Homo sapiens (man)

C: Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C: Accession: A54821

R: Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.

Cell 78, 739-750, 1994

A: Title: ICH-1, an Ice/Ced-3-related gene, encodes both positive and negative regulators

A: Reference number: A54821; MUID: 94373611; PMID: 8087842

A: Accession: A54821

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-435 <MAN>

A: Cross-references: GB:U13021; NID:9537291; PID:9537292

C: Keywords: alternative splicing; apoptosis

Query Match 22.5%; Score 328.5; DB 2; Length 435;

Best Local Similarity 27.9%; Pred. No. 4.5e-19;

Matches 83; Conservative 62; Mismatches 120; Indels 33; Gaps 7;

2 ENTENSVDK-----STNLEPKIHGSESDSGISLSDNSYKNDYFPMGLCTIINKNF 55

142 DIVEHSLNRKDGPCVLDQVRCPTREFYQTHFOL-----AYRLQSRPRGLALVLSNVH 193

56 HKSTMTSGSTVDVAANLRETFRNLYEVNRKNDLTREIEVLMADVSK-EDHSKRSF 114

194 TGERLEFRSGGDVHDSTLVTFKLGIVHYVLCDDTAQDMQKLDNFAHRAVTDSC 253

115 VCVLLSHGEEGIIFTNGP-VDLKITNFRGDRCSLTGKPKLFIIOACRGTELDGCI- 172

254 IVALLSHGEVGIYGVDCGLQLOEVEFOLFDMANCPISLNKPKMFITQACRGDETGRVD 313

173 -----ETDSVDDMACHKITPVEADFLYASTAPGYISMRNSKDGSEFIO 218

314 OODGNHNAHSGPCESDAC-KEKLRPMRLPTRSDMIGCAJCKGTAMNTKGSWYIA 372

219 LCAMLKOYADKLEFPHILTRVNRKVAATEPESFSDATFAKKOIPCTIVMLTRELVEY 276

373 LAOVSEKACOMHNAVDMYKVALI-KDEGYIAPGTETFRCKEMSEYSCSTLCRHLYLF 429

RESULT 10

JC6507

caspase-2 - rat

C: Species: Rattus norvegicus (Norway rat)

C: Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C: Accession: JC6507

R: Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.

Gene 202, 127-132, 1997

A: Title: Cloning and expression of the cDNA encoding rat caspase-2.

A: Reference number: JC6507; MUID: 98087427; PMID: 9427555

A: Accession: JC6507

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-452 <SAT>

A: Cross-references: GB:U7933; NID:92769705; PIDN: AAB96379.1; PID: 92769706

Query Match 22.4%; Score 327.5; DB 2; Length 452;

Best Local Similarity 30.6%; Pred. No. 5.6e-19;

Matches 79; Conservative 53; Mismatches 107; Indels 19; Gaps 5;

36 SYKNDYDEMGLCTIINKNFKHSTGMRSSTVDVAANLRETFRNLYEVNRKNDLTREE 95

191 AYRLQSPRGIALVMSVNHFGKEDLEFRSGDVDDHTLVTFKLGIVHYVLCDDTAQ 250

96 IVELMDVSK-EDHSKRSSEVCVLLSHGEEGIIFTNGP-VDLKITNFRGDRCSLTG 153

251 MQEKLQNFADLPARVYDSCVALLSHGVEGIGYGVCKLQLOEVEFRLFNANCPISLN 310

154 KPKLFIIOACRGTELDGCI-----ETDSVDDMACHKITPVEADFLYAYS 198

311 KPMKFIIOACRGDETRDGVDDQDGKNAQSPCEESDAGKELKMK-RLPTRSDMIGCA 369

199 TAPGYISMRNSKDGSEWFOISLCAMLKOYADKLEFPHILTRVNRKVAATEPESFSDATFHA 258

370 CLGNAMRNTKRSWYIEALTOVFSERACDMHVAIDMYKVALI-KEREGYAPGTETFRH 428

259 KKOIPCLVSMITELVLY 276

429 CKEMSEYSCSTLCRHLYLF 446

RESULT 11

T43633

N: Contains: caspase 1B

C: Species: Caenorhabditis elegans

C: Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C: Accession: T43633; T43636

R: Shaham, S.

J. Biol. Chem. 273, 35109-35117, 1998

A: Title: Identification of multiple Caenorhabditis elegans caspases and their potent

A: Reference number: Z22587; MUID: 99074291; PMID: 9857046

A: Accession: T43633

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-536 <SHA>

A: Cross-references: EMBL:AF088285; NID:94063367; PIDN: AAC98292.1; PID: 94063368

A: Accession: T43636

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 269-536 <SH2>

A: Cross-references: EMBL:AF088286; NID:94063369; PIDN: AAC98293.1; PID: 94063370

C: Genetlcs: 1

A: Gene: csp-1

A: Map position: 2

C: Function: probably acts in proteolytic cascades to regulate processes such as p.

C: Description: probably acts in proteolytic cascades to regulate processes such as p.

C: Keywords: cysteine proteinase; hydrolase

Query Match 21.2%; Score 310.5; DB 2; Length 536;

Best Local Similarity 29.5%; Pred. No. 1.7e-17;

Matches 76; Conservative 62; Mismatches 91; Indels 29; Gaps 9;

37 YKMDYDEMGLCTIINKNFKHSTGMRSSTVDVAANLRETFRNLYEVNRKNDLTREE 96

285 YEKNSNPRTGTVLLISNENF---KNMERVGTGDEVNLTFLFKLOLYTVICKRNLEAESM 341

QY 204 YSMRNSKDSGWFIOISLCAMLKOYADKLEFMHILTRVNRKVAPEFSFDPATHAKQIP 263
DB 176 IAYRHDOGSCFIOQLVDFETK--RKGHILELLETVTRRMA-EAEVLQ---ECKARKTNP 229
QY 264 CIVSMUTKELY 274
DB 230 EIQSTLRKRRLY 240

RESULT 15
A46495

IL-1 beta convertase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A46495; A47258; I48911

R:Nett, M.A.; Gerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Jenkins, N.A.; C

J. Immunol. 149, 3254-3259, 1992.

A:Title: Molecular cloning of the murine IL-1 beta converting enzyme cDNA.

A:Reference number: A46495; MUID:93056487; PMID:1431103

A:Accession: A46495

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-402 <NET>

A:Cross-references: GB:I03799; NID:q198379; PIDN:AAA39306.1; PID:q198380

A:Note: Sequence extracted from NCBI backbone (NCBIP:117473)

R:Mollineaux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Lamjuno, G.; Chin, J.; G

ard, A.D.; Thornberry, N.A.; Kostura, M.J.

Proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993

A:Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages requires a stru

A:Reference number: A47258; MUID:93189587; PMID:8446594

A:Accession: A47258

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-187, 189-402 <MOL>

A:Experimental source: macrophage

A:Note: Sequence extracted from NCBI backbone (NCBIP:126931)

R:Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Mollineaux, S.M.

Genomics 20, 474-481, 1994

A:Title: The structure and complete nucleotide sequence of the murine gene encoding Inte

A:Reference number: A54264; MUID:94307735; PMID:8034321

A:Accession: I48911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: "MAV", 7-402 <RES>

A:Cross-references: EMBL:U04269; NID:q476217; PIDN:AAA56992.1; PID:q476218

C:Genetics:

A:Introns: 6/1: 92/1; 113/1; 150/3; 208/3; 287/1; 334/1; 370/3

Query Match

16.9%; Score 247.5; DB 2; Length 402;

Best Local Similarity 29.0%; Pred. No. 1.6e-12;

Matches 88; Conservative 46; Mismatches 124; Indels 45; Gaps 11;

QY 6 NSVDSKSIKNEPKIHSESDSISLDSNYKM-----DYPEMG-----LCIIINN 52
DB 110 SSSSTKEEKNEDGTFPGTLGTLPKCPLEKAKQKWKENSEIYPIIMNTTTRTLALICN 169
QY 53 KNFEKSTGMTSRSGTDVDAANLRFTFRNLKYEVNRKNLDTREIYELMRDYSK-EDHSKR 111
DB 170 TEPQH---LSRPVGAQVLDREKLLLEDIGTYVKYKENLTALAEVKEVKEFAACEPHKTS 226
QY 112 SSFVCVLLSHG-EEGIIFGT--NGPVDLKITNFR--GDRCRSITGCKPLFIIOACRG 165
DB 227 DSTFLVFMHSHGIEGICGTYTSNEVSDILKVDITFQMMNTLCKPSLKDKPKVITIIQACRG 286
QY 166 TELDQGITDS-----GVDDDMACHKIPYEADEFIAYSTAPGYYSNRNSKDSG 214
DB 287 EKQGVLLKDKDSVDEEDFLDALPEDEGDIKKAHIEKDFIACSSPTPDNVSMRHPYRGSL 346
QY 215 FIOSLCAMLKOYADKLEFMHILTRVNRKVAPEFSFDPATHAKQIPCIYSM-LTKEL 273
DB 347 FIESLIKMKREYAMSCD---LEDIFRKVYRPSFEOPEF-----RLQMPTRADVITLTKRF 396

QY 274 YFY 276
DB 397 YLF 399

Search completed: December 2, 2002, 12:57:09
Job time: 17.2828 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 9.55172 Seconds

(without alignments)
1202,814 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463

Sequence: 1 MENTENSVDKSIKNEPKI.....AKKOIPCVSMLEKELYFH 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1460	99.8	277	1	ICE3_HUMAN
2	1317	90.0	277	1	ICE3_HUMAN
3	1293	88.4	277	1	ICE3_HUMAN
4	1293	88.4	277	1	ICE3_HUMAN
5	786.5	53.8	282	1	ICE3_HUMAN
6	748.5	51.2	303	1	ICE3_HUMAN
7	726.5	49.7	303	1	ICE3_HUMAN
8	726.5	49.7	303	1	ICE3_HUMAN
9	517.5	35.4	293	1	ICE3_HUMAN
10	517.5	35.4	293	1	ICE3_HUMAN
11	502.5	34.3	339	1	ICE3_HUMAN
12	470	32.1	299	1	ICE3_HUMAN
13	469	32.1	299	1	ICE3_HUMAN
14	421	28.8	479	1	ICE3_HUMAN
15	410	28.0	503	1	ICE3_HUMAN
16	381.5	26.1	516	1	ICE3_HUMAN
17	362	24.7	496	1	ICE3_HUMAN
18	356.5	23.0	435	1	ICE3_HUMAN
19	336.5	23.0	435	1	ICE3_HUMAN
20	328.5	22.9	435	1	ICE3_HUMAN
21	321	21.5	521	1	ICE3_HUMAN
22	274.5	18.8	242	1	ICE3_HUMAN
23	274	18.7	257	1	ICE3_HUMAN
24	266.5	18.2	386	1	ICE3_HUMAN
25	265.5	18.1	410	1	ICE3_HUMAN
26	259.5	17.7	382	1	ICE3_HUMAN
27	254.5	17.4	409	1	ICE3_HUMAN
28	253	17.3	402	1	ICE3_HUMAN
29	250	17.1	405	1	ICE3_HUMAN
30	247.5	16.9	402	1	ICE3_HUMAN
31	246.5	16.8	377	1	ICE3_HUMAN
32	239	16.3	312	1	ICE3_HUMAN
33	235.5	16.1	377	1	ICE3_HUMAN

34	234.5	16.0	404	1	IBCB_CANPA
35	232.5	15.9	418	1	ICES_HUMAN
36	222.5	15.2	404	1	IBCB_HUMAN
37	217.5	14.9	373	1	ICEB_MOUSE
38	213.5	14.6	404	1	IBCB_PIG
39	202	13.8	484	1	CFLA_MOUSE
40	183	12.5	480	1	CFLA_HUMAN
41	96	6.6	536	1	FYN_XIPHE
42	93	6.4	533	1	FYN_CHICK
43	92.5	6.3	5255	1	BACA_BACLI
44	90.5	6.2	533	1	FYN_MOUSE
45	88	6.0	536	1	FYN_HUMAN

ALIGNMENTS

RESULT 1	ID	ICE3_HUMAN	STANDARD:	PRT:	277 AA.
AC	P42574	ICE3_HUMAN			
DT	01-NOV-1995	(Rel. 32, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Apoptain precursor (PC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) (SCA-1).				
DE	CASP3 OR CPP32.				
GN	CASP3 OR CPP32.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
CC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).				
RC	TISSUE=T-cell;				
RC	TISSUE=T-cell;				
RX	MEDLINE=95074098; PubMed=7983002;				
RA	Fernandes-Alnemri T., Litwack G., Alnemri E.S.;				
RT	"CPP32, a novel human apoptotic protein with homology to				
RT	Caenorhabditis elegans cell death protein Ced-3 and mammalian				
RT	Interleukin-1 beta-converting enzyme.";				
RL	J. Biol. Chem. 269:30761-30764(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=95292347; PubMed=7774019;				
RA	Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,				
RA	Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;				
RT	"Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable				
RT	protease that cleaves the death substrate poly(ADP-ribose)."				
RL	Cell 81:801-809(1995).				
RN	[3]				
RP	SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.				
RC	MEDLINE=95319529; PubMed=7596430;				
RA	Nicholson D.W., Ali A., Thornberry N.A., Vallancourt J.P., Ding C.K.,				
RA	Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,				
RA	Mundler N.A., Rayn S.M., Smulson M.E., Yamin T.-T., Li V.L.,				
RA	Miller D.K.;				
RT	"Identification and inhibition of the ICE/CED-3 protease necessary				
RT	for mammalian apoptosis.";				
RL	Nature 376:37-43(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.				
RC	MEDLINE=9626352; PubMed=8673606;				
RA	Rolonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,				
RA	Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vallancourt J.P.,				
RA	Thornberry N.A., Becker J.W.;				
RT	"The three-dimensional structure of apoptin/CPP32, a key mediator of				
RT	apoptosis.";				
RL	Nat. Struct. Biol. 3:619-625(1996).				
RN	[5]				
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.				
RC	MEDLINE=97197830; PubMed=9045680;				
RA	Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,				

RA Priestle J.P., Tomaselli K.J., Grutter M.G.:
 RT "Structure of recombinant human CPP32 in complex with the
 RL tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone."
 J. Biol. Chem. 272:6539-6547(1997).
 [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RP MEDLINE-20283632; PubMed-10821855;
 RX Lee D., Long S.A., Adams J.L., Chan G., Valdivia K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., Demolf W.E., Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Hallwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
 RA Johnson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.:
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality."
 RL J. Biol. Chem. 275:16007-16014(2000).
 [7]
 RN PROCESSING.
 RP MEDLINE-96353838; PubMed-8755496;
 RX Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.:
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 [8]
 RN CLEAVAGE OF HUNTINGTIN.
 RP MEDLINE-96331285; PubMed-8696339;
 RX Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thorberry N.A.,
 RA Vallancourt J.P., Hayden M.R.:
 RT "Cleavage of huntingtin by apolipin, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract."
 RL Nat. Genet. 13:442-449(1996).
 [9]
 RN - FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES SEROL REGULATOR
 CC ELEMENT BINDING PROTEIN (SREBP) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
 CC CLEAVAGE OF HUNTINGTIN.
 CC - ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
 CC - SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
 CC - SUBCELLULAR LOCATION: Cytoplasmic.
 CC - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
 CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW
 CC IN TESTIS. ALSO FOUND IN MANY CELL LINES. HIGHEST EXPRESSION IN
 CC CELLS OF THE IMMUNE SYSTEM.
 CC - PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as their content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL, U13737; AA65015.1;
 DR EMBL, U13738; AA60355.1;
 DR EMBL, U26943; AAA74929.1;
 DR PDB, 1PAU; 07-JUN-97.
 DR PDB, 1CP3; 24-DEC-97.
 DR PDB, 1GFV; 23-JUN-00.
 DR MEROPS, C14.003;
 DR Genew, HGNC:1504; CASP3.

DR MIN; 600636;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILICENZYME.
 DR SMART; SM00115; CASP; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; CASPASE; P20; 1.
 KW 3D-structure.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT ACT_SITE 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARIANT 190 190 D->E (IN ISOFORM BETA).
 FT /FTID=VAR_001401.
 FT /FTID=VAR_001401.
 SQ SEQUENCE 277 AA; 31594 MW; 8E34DD2ACE6E6F64B CRC64;
 Query Match 99.8%; Score 1460; DB 1; Length 277;
 Best Local Similarity 99.6%; Pred. No. 1.7e-115;
 Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MENTENSVDKSKIKNLEPKIIGSESDSGISLNSYKMDYPEKGLCTIINKNFHKSTG 60
 DB 1 MENTENSVDKSKIKNLEPKIIGSESDSGISLNSYKMDYPEKGLCTIINKNFHKSTG 60
 QY 61 MTSRSGTDVDAANLRETFRNLYKVEVRNKNDFREIYELMRDVSKEHRSKSSFCVLLS 120
 DB 61 MTSRSGTDVDAANLRETFRNLYKVEVRNKNDFREIYELMRDVSKEHRSKSSFCVLLS 120
 QY 121 HGEGRITFGNGPVDLKKITNFFRGDCRSITGPKFLITQACGTEDLDCIETDSGYDD 180
 DB 121 HGEGRITFGNGPVDLKKITNFFRGDCRSITGPKFLITQACGTEDLDCIETDSGYDD 180
 QY 181 DMACHKIPVADFLYASTAPGYSMNSKDGSMFISLCLAMLRQYADKLEFMIILFRVN 240
 DB 181 DMACHKIPVADFLYASTAPGYSMNSKDGSMFISLCLAMLRQYADKLEFMIILFRVN 240
 QY 241 RKVATFEFSFDPATFPAKKOIPCIYVSMLEKELYFH 277
 DB 241 RKVATFEFSFDPATFPAKKOIPCIYVSMLEKELYFH 277
 RESULT 2
 ID ICE3_RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; Q62993; P97699;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96358624; PubMed-8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.:
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3."
 RL Oncogene 13:749-755(1996).

RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RX TISSUE-Ovary; PubMed-7588240;
 RA Flaws J.A., Kugu K., Tribovich A.M., Desanti A., Tilly K.I.,
 RA Hirschfeld A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RT of the ovarian follicle.";
 RL Endocrinology 136:5042-5053(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RA MEDLINE-97184204; PubMed-9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostek P. Jr., Polster G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-1-beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569(1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 17 Kda (P17) AND A 12 Kda (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
 CC BUT NOT IN KIDNEY OR TESTIS.
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
 CC ADULT BRAIN.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sdb.ch).
 CC -----
 DR EMBL; U49930; AAC52765.1; -
 DR EMBL; U34685; AAC52261.1; -
 DR EMBL; U84410; AAB41792.1; -
 DR EMBL; U58656; AAB02722.1; -
 DR HSSP; P42574; IPRU.
 DR MEROPS; C14.003; -
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00655; ICE_p20; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.

KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT ACT_SITE 25 29
 FT CONFLICT 170 170
 FT CONFLICT 178 178
 FT CONFLICT 182 182
 FT CONFLICT 187 187
 FT CONFLICT 190 190
 FT CONFLICT 199 199
 FT CONFLICT 211 211
 FT CONFLICT 236 236
 FT CONFLICT 245 245
 FT CONFLICT 245 245
 SQ SEQUENCE 277 AA; 31491 MW; ADABP418E2507402 CRC64;
 Query Match 90.0%; Score 1317; DB 1; Length 277;
 Best Local Similarity 89.2%; Pred. No 1.8e-103;
 Matches 247; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MENTENSVDKSKINLEPKIIGSESDSGISLDSYKMDYPENGLCTIINKNFKSTG 60
 DB 1 MDNNETSVDSKINNFETKTIHSGSKSDSGIYLSYKMDPEMGLCTIINKNFKSTG 60
 QY 61 MTSAGSDVDVAAANREFRNKIYVRKNNDLTREIYELMDVSKEDSKSSFEVCVLLS 120
 DB 61 MSANGTDVDAANLREFFMALKEVRKNNDLTREIMELMDVSKEDSKSSFEVCVLLS 120
 QY 121 HGEGLIFGTNGPVDLKITNFEFGDRCSLTGPKFIIOACGTETDGLDGTGVD 180
 DB 121 HGDGVIETGNGPVDLKITNFEFGDVCRLTGPKFIIOACGTETDGLDGTGVD 180
 QY 181 DMACHKIPVADFLYASTAGYVSMRNSKDGSWFIOSLCAMLQYADKLEFMILTRVN 240
 DB 181 DMACQKIPVADFLYASTAGYVSMRNSKDGSWFIOSLCAMLKLYAHKLEFMILTRVN 240
 QY 241 RKVATEFESFDPATFRAKQIPCIYSMLTKELYFYH 277
 DB 241 RKVATEFESFDPATFRAKQIPCIYSMLTKELYFYH 277
 RESULT 3
 ID ICE3_CRILLO STANDARD; PRT; 277 AA.
 AC 060431;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RA MEDLINE-96183185; PubMed-8605870;
 RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
 RT CPP32 during apoptosis.";
 RL EMO J. 15:1012-1020(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY

CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPB32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27463; AAB01511.1; -
DR HSRP: P42574; IPR0.
DR MEROPS: C14.003; -
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBENZYM.
DR SMART: SM00115; CASP. 1.
DR PROSITE: PS01122; CASPASE_CYS. 1.
DR PROSITE: PS01121; CASPASE_HIS. 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9 BY SIMILARITY.
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 88.4%; Score 1293; DB 1; Length 277;
Best Local Similarity 87.0%; Pred. No. 1.8e-101;
Matches 241; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MENTENVDSKSIKLEPKTIHSESDSGTSLDSYKMDYPMGCLTIINKNKFKSTG 60
DB 1 MENTENVDSKSIKLEPKTIHSESDSGTSLDSYKMDYPMGCLTIINKNKFKSTG 60
QY 61 MTSKSGTDVDAANLRETFRNLYEVNRKNDLTREIYEIAMDVSKEDSKRSSFCVLLS 120
DB 61 MTPRSGTDVDAAKLRETFRNLYEVNRKNDLTREIYEIAMDVSKEDSKRSSFCVLLS 120
QY 121 HGESEGIIFGNGVDLKKITNFGRDRCSTLTKPKLFTI0ACRGTELDGCIETDSGYD 180
DB 121 HGESEGIIFGNGVDLKKITNFGRDRCSTLTKPKLFTI0ACRGTELDGCIETDSGYD 180
QY 181 DMACCHKRPVADFLYASTAGYYSMNNSDGSFIOISLCAMLKQYADKLEFHHILRVN 240
DB 181 DMACCHKRPVADFLYASTAGYYSMNNSDGSFIOISLCAMLKQYADKLEFHHILRVN 240
QY 241 RKVATEFESEFDPATFHAARKQIPCIYSLTKELFYH 277
DB 241 RKVATEFESEFDPATFHAARKQIPCIYSLTKELFYH 277
RESULT 4
ICE3_MOUSE
ID ICE3_MOUSE STANDARD: PRT: 277 AA.

AC P70677; 008668.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPB32) (Yama
DE protein) (CPB-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
GN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNelece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling Interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
RA van Ioo G., Molens F., Schotte P., van Gieken W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
RL -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RL RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
RL PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PAR) AT A
RL 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
RL ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
RL HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
RL CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
RL CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
RL -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
RL (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LIVER,
CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
CC TESTIS.
CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEPTASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----


```

CC -----
DR EMBL: U54803; AAC52768.1; -
DR EMBL: U54802; AAC52768.1; JOINED.
DR EMBL: U49929; AAC52764.1; -
DR EMBL: D86352; BAA21727.1; -
DR EMBL: Y13086; CAA3528.1; -
DR EMBL: U19522; AAC53196.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -.
DR MGD: MGI:107739; Casp3.
DR InterPro: IPR002388; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR Hydrolase: Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT CONFLICT 51 51
FT CONFLICT 84 84
FT CONFLICT 95 95
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 135 135
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;

```

```

Query Match      88.4%; Score 1293; DB 1; Length 277;
Best Local Similarity 86.6%; Pred. No. 1.8e-101;
Matches 240; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

```

```

QY 1 MENTNSVSKSKIKLEPPIIHGSESDGISLNDYKMDYDEMGLCTIINNNKFKSTG 60
DB 1 MENTNTSDSKSINNFEVATIHGSKSVDSGIYLDSSYKMDYDEMGLCTIINNNKFKSTG 60
QY 61 MTSRSGTVDANLRETFRNLYEVRNKNLDTREIIVELMRVSKEDHSKRSFVCVLLS 120
DB 61 MSSRSGTVDANLRETFRNLYEVRNKNLDTREIIVELMRVSKEDHSKRSFVCVLLS 120
QY 121 HGEBCITFGNGPVDLKKITNEFFRGDRCSLTGPKPLFIIOACRGTELDGCIETDSGVDD 180
DB 121 HGDEGVIVGTNGPVDLKKITNEFFRGDRCSLTGPKPLFIIOACRGTELDGCIETDSGVDD 180
QY 181 DMACHKTIIVEADFLAYASTARPGYISWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
DB 181 EMACKTIIVEADFLAYASTARPGYISWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESFSDATFFHAKKOIPCIYVSMILTKELYFH 277
DB 241 RKVATEFESFSDATFFHAKKOIPCIYVSMILTKELYFH 277

RESULT 5
ID ICE3_XENLA STANDARD: PRT: 282 AA.
AC P55866:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (caspase-3)
DE (CASP-3) (XCP32).
GN CASP3.
OS Xenopus laevis (African clawed frog).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Taolte Y., Nakajima K.;
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RT myoblastic cell line derived from tadpole tail."
RL J. Biol. Chem. 272:5122-5127(1997)
CC -1- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF
CC APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE
CC (PAR) AT A 216-ASP-1-GLY-217 BOND (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12)
CC SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE PRECURSOR
CC SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AND PROBABLY BY
CC OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D89784; BAA14018.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -.
DR InterPro: IPR002388; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT CHAIN 187 282
FT ACT_SITE 131 131
FT ACT_SITE 174 174
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

```

```

Query Match      53.8%; Score 786.5; DB 1; Length 282;
Best Local Similarity 54.2%; Pred. No. 6.1e-59;
Matches 156; Conservative 40; Mismatches 73; Indels 19; Gaps 5;

```

```

QY 1 MENTNSV-----DSKIKNLEPKIHHGSESD-----SGISLNDYKMDYDEMGLCTI 49
DB 1 MESQNGVYGGDADATDAKYEFTIOPRSIONCDLDERKTFKFAHLNRYNYPDEMGLCI 60
QY 50 INNNFKHSTGMTSRSGTVDANLRETFRNLYEVRNKNLDTREIIVELMRVSKEDHS 109
DB 61 INNNKFNH-SSNNAVRNGTVDALKLHETFTGLGYEVMVCNDKSSDILGKLTISEDHS 119
QY 110 KRSSFVCVLLSHGEE-GILFTNGPVDLKKITNEFFRGDRCSLTGPKPLFIIOACRGTEL 168
DB 120 KRSSFVCALLSHGEDGSGCGVDVPIHINKNLDTREIIVELMRVSKEDHSKRSFVCVLLS 179
QY 169 DCGIETDSCVDDMACHKITPVADFLAYASTARPGYISWRNSKDSWFIQSLCAMLKQYAD 228
DB 180 DSGIETDSCSEPREETORIPVADFLAYASTARPGYISWRNSKDSWFIQSLCAMLKQYAD 239
QY 229 KLEFMHILTRVNRKVATEFESFSDATFFHAKKOIPCIYVSMILTKELYF 276

```


Db 240 HLEIDILQITCVNHNVALDFE-----TFHAKQIPCVWSMLTKSPYFF 281

RESULT 6

ICET_MOUSE STANDARD; PRT; 303 AA.

AC P97864; 008669; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic protease Mch-3).

GN CASP7 OR MCH3 OR LICE2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE=97224489; PubMed=9070923;

RA Juan T.-C., McNeice I.K., Argento J.M., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.;

RT "Identification and mapping of Casp7, a cysteine protease resembling CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";

RL Genomics 40:86-93(1997).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=9736307; PubMed=9125129;

RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I., Momoi T.;

RT "Wortmannin enhances CPP32-like activity during neuronal differentiation of P19 embryonal carcinoma cells induced by retinoic acid.";

RL Biochem. Biophys. Res. Commun. 232:192-197(1997).

RN (3)

RP SEQUENCE FROM N.A.

RX STRAIN=C3H/An;

RX MEDLINE=97190206; PubMed=9038361;

RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I., van Loo G., Molemans F., Schotte P., Van Clekeinge W., Beyaert R., Fiers W.;

RT "Characterization of seven murine caspase family members.";

RL FEBS Lett. 403:61-69(1997).

RN (4)

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL REGULATOR ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).

CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO EXPRESSION IN THE BRAIN.

CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

DR EMBL: U67321; AAC53068.1; ALT_INIT.

DR EMBL: D86353; BAA19730.1; -

DR EMBL: Y13088; CAA73530.1; -

DR EMBL: BC005428; AAH05428.1; -

DR HSSP: P42574; 1PAU.

DR MEROPS: C14.004; -

DR MGD: MGI:109383; Casp7.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE_P10.

DR InterPro: IPR001309; ICE_P20.

DR Pfam: PF00655; ICE_P10; 1.

DR Pfam: PF00656; ICE_P20; 1.

DR PRINTS: PR00376; TLICENZYME.

DR SMART: SM00115; CASC; 1.

DR PROSITE: PS01122; CASPASE_CYC; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

KW Hydrolase; Thiol protease; Zymogen; Apoptosis.

FT PROPEP 1 23

FT CHAIN 24 198

FT PROPEP 199 206

FT CHAIN 207 303

FT ACT_SITE 144 144

FT ACT_SITE 186 186

FT CONFLICT 10 11

FT CONFLICT 45 45

FT CONFLICT 48 49

FT CONFLICT 48 49

FT SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match 51.2%; Score 748.5; DB 1; Length 303;

Best Local Similarity 59.5%; Pred. No. 1e-55; Matches 144; Conservative 36; Mismatches 59; Indels 3; Gaps 1;

QY 37 YKDYPMGGLCIITNNKFNHSTGTSRSGTDVAANLRETFRNLYKVEVRKNDLTREEI 96

DB 60 YRDFQMGKCIITNNKFNHSTGTSRSGTDVAANLRETFRNLYKVEVRKNDLTREEI 119

QY 97 VELRDVSKEDHSKRSSFVCLLSHGEGIIETGNGPVLDLKITNFGRGCRSLTGKPK 156

DB 120 QDLIRKASEEDHSNACFACVLLSHGEGEDLYGKGVTPYKDLTAHFRGDRCKLTLEKPK 179

QY 157 LFTIACRGTELDGIGTSDGVDDMAC---HKIPVADFLIYASTAGIYSWRNKGDS 213

DB 180 LFTIACRGTELDGIGTSDGVDDMAC---HKIPVADFLIYASTAGIYSWRNKGDS 239

QY 214 WFIOSLCAMEKQYADKLEFPHIILTRVNRKVAETEESEFSDATFPAKQIPCIYSMLTEL 273

DB 240 WFIOALCSILNHEKQLEHQLILTRVNDRAVRHESQSDPRFNEKKQIPCVWSMLTEL 299

QY 274 YF 275

DB 300 YF 301

RESULT 7

ICET_MOUSE STANDARD; PRT; 303 AA.

AC P55214; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Caspase-7 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 3) (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2) (SCA-2).

GN CASP7 OR MCH3.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.

OX NCBI_TaxID=10036;

RN (1)

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

```

RC STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pal J.-T., Brown M.S., Goldstein J.L.;
RT "Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 20 KDA (P20) AND A 11 KDA (P11) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U47332; AAC52595.1; -.
DR HSSP: P42574; IPAU.
DR MEROPS: C14.004; -.
DR InterPro: IPR002338; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR Pfam: PF00657; ICE_P20; 1.
DR PRINTS: SM00115; CASC. 1.
DR SMART: SM00115; CASC. 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR Hydrolase: Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 1 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29355D9098448 CRC64;

Query Match 49.7%; Score 726.5; DB 1; Length 303;
Best Local Similarity 58.3%; Pred. No. 7,3e-54;
Matches 141; Conservative 35; Mismatches 63; Indels 3; Gaps 1;

```

```

OY 274 YF 275
II
DB 300 YF 301

RESULT 8
ICE7_HUMAN
ID ICE7_HUMAN STANDARD: PRT; 303 AA.
AC P55210; 013364; 096BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
GN CASP7 OR MCH3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinaiyan A.M., Hudson P.L., Wang J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96147144; PubMed=857622;
RA Lipkpe J.A., Gu Y., Sarnecki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homology 1, a novel
RT cysteine protease similar to CPP32."
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandez-Alnemir T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaselli K.J., Wang L.C., Yu Z., Croce C.M., Salveson G.,
RA Earnshaw W.C., Litwack G., Alnemir E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=9633838; PubMed=8755496;
RA Fernandes-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemir E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains."
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY

```

[illegible]

DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10: 1.
 DR Pfam: PF00656; ICE_p20: 1.
 DR PRINTS: PRO0376; ILIBCENTIME.
 DR SMART: SM00115; CASc: 1.
 DR PROSITE: PS01122; CASPASE_CYS: 1.
 DR PROSITE: PS01121; CASPASE_HIS: 1.
 DR PROSITE: PS50207; CASPASE_P10: 1.
 DR PROSITE: PS50208; CASPASE_P20: 1.
 KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 5
 FT CHAIN 6 162 BY SIMILARITY.
 FT PROPEP 163 176 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
 FT CHAIN 177 276 BY SIMILARITY.
 FT ACT_SITE 104 104 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
 FT ACT_SITE 146 146 BY SIMILARITY.
 FT ACT_SITE 146 146 BY SIMILARITY.
 SQ SEQUENCE 276 AA; 31595 MW; 5965DE9321126B6C CRC64;

Query Match 36.0%; Score 526; DB 1; Length 276;
 Best Local Similarity 41.4%; Pred. No. 4,4e-37;
 Matches 104; Conservative 42; Mismatches 93; Indels 12; Gaps 1;

OY 37 YKMDYEMGICIIINKNHFKSTGTSRSGTDVDAANLREFFNLYEVANKNDLTFEEI 96
 DB 20 YKMDHRRGVALIENHERFWMILTPERRCTADRNLTFRFSDLGEVCFNDLAEEL 79
 OY 97 VELMDVSKEDHSKRSSFVCLSHGEEGIIIFGTNGPVDLKITNFPRGDRCSLTKPK 156
 DB 80 LKIHVEVSTSHADDCFLSHGEGNHVYADAKIEIQTILGFGKCSLYGKPK 139
 OY 157 LFTIACRGTETDCGIIETDSCVD-----DDMACHKIPVADFLVAVSTAPGY 204
 DB 140 IFTIACRSGSDHVPVPLDWDVNDQTKLDNVTQVAAVYTLTPAGADFLMCYSVAEGY 199
 OY 205 SWRNSKDSWFTIOLSCAMLKQYADKLEFMHILTRVNRKVAEFESFSDATFPAKKOIPC 264
 DB 200 SHRETVNGSWIYDLCCEMLARGSSLEFTELLTLVNRKVSORRVDFCKDPDAIGKKOVP 259
 OY 265 IYSMLTKELYF 275
 DB 260 FASMLTKLHF 270

RESULT 10
 ICE6_HUMAN STANDARD: PRT; 293 AA.
 AC P55212;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
 GN CASP6 OR MCH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=95316841; PubMed=7796396;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene family.";
 RL Cancer Res. 55:2737-2742(1995).
 RP [2]
 RC PROCESSING.
 RP TISSUE=Lymphocytes;
 RX MEDLINE=97059171; PubMed=8900201;
 RA Stinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RT "The Ced-3/Interleukin 1beta converting enzyme-like homolog Mch6 and

RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic mediator CPP32.";
 RL J. Biol. Chem. 271:27099-27106(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE) POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: CYTOSOLSMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA (SHOWN HERE) AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM DOES NOT SEEM TO HAVE PROTEOLYTIC ACTIVITY.
 CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: U20536; AAC50168.1; -;
 CC EMBL: U20537; AAC50169.1; -;
 CC HSSP: P42574; 1PAU.
 CC DR HMRPS: C14.005; -;
 CC DR Genew: HGNC:1507; CASP6.
 CC DR MIM: 601532; -;
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10: 1.
 DR Pfam: PF00656; ICE_p20: 1.
 DR PRINTS: PRO0376; ILIBCENTIME.
 DR SMART: SM00115; CASc: 1.
 DR PROSITE: PS01122; CASPASE_CYS: 1.
 DR PROSITE: PS01121; CASPASE_HIS: 1.
 DR PROSITE: PS50207; CASPASE_P10: 1.
 DR PROSITE: PS50208; CASPASE_P20: 1.
 KW Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 FT PROPEP 1 23
 FT CHAIN 24 179 CASPASE-6 SUBUNIT P18.
 FT PROPEP 180 193
 FT CHAIN 194 293
 FT ACT_SITE 121 121 CASPASE-6 SUBUNIT P11.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARSPLIC 14 102 MISSING (IN ISOFORM BETA).
 SQ SEQUENCE 293 AA; 33409 MW; BD9204E23CE1F670 CRC64;

Query Match 35.4%; Score 517.5; DB 1; Length 293;
 Best Local Similarity 41.1%; Pred. No. 2,4e-36;
 Matches 104; Conservative 42; Mismatches 94; Indels 13; Gaps 1;

OY 37 YKMDYEMGICIIINKNHFKSTGTSRSGTDVDAANLREFFNLYEVANKNDLTFEEI 96
 DB 37 YKMDHRRGVALIENHERFWMILTPERRCTADRNLTFRFSDLGEVCFNDLAEEL 96
 OY 97 VELMDVSKEDHSKRSSFVCLSHGEEGIIIFGTNGPVDLKITNFPRGDRCSLTKPK 156
 DB 97 LKIHVEVSTSHADDCFLSHGEGNHVYADAKIEIQTILGFGKCSLYGKPK 156
 OY 157 LFTIACRGTETDCGIIETDSCVD-----ETDSDVDDMACHKIPVADFLVAVSTAPGY 203
 DB 157 IFTIACRSGSDHVPVPLDWDVNDQTEKLDNVTQVAAVYTLTPAGADFLMCYSVAEGY 216
 OY 204 YSRNSKDSWFTIOLSCAMLKQYADKLEFMHILTRVNRKVAEFESFSDATFPAKKOIPC 263
 DB 217 YSHRETVNGSWIYDLCCEMLARGSSLEFTELLTLVNRKVSORRVDFCKDPDAIGKKOVP 276
 OY 264 CIVSMLTKELYF 276
 DB 260 FASMLTKLHF 270

Db 277 CFASMLTKLHFF 289

```
RESULT 11
ICE_DROME
ID ICE_DROME STANDARD: PRT: 339 AA.
AC 001382: 09VAH1: 35, Created)
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (drice).
GN ICE OR CG7788.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7221;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97327558; PubMed=9184225;
RA Fraser A.G., Evan G.I.;
RT "Identification of a Drosophila melanogaster ICE/ced-3-related
RT protease, drice".
RL EMBO J. 16:2805-2813(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ageton L.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brocktein P., Brottier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dushin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodaira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson K.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA She B.C., Sideri-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton W., Strong M., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:185-2195(2000).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOWNSTREAM OF RPR.
CC CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITRO.
CC -1- SUBUNIT: HETERODIMER OF A 21 KDa (P21) AND A 12 KDa (P12) SUBUNIT.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES WHERE APOPTOSIS
CC OCCURS.
```

```
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

DR EMBL: Y12261; CAAT72937.1; -
DR EMBL: AE003771; AAF56939.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.015; -
DR FlyBase: FBgn0019972; Ice.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBENZTYME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; zymogen; Apoptosis.
FT PROPEP 1 28
FT CHAIN 29 217
FT PROPEP 218 230
FT CHAIN 231 339
FT ACT_SITE 169 169
FT ACT_SITE 211 211
FT CONFLICT 151 151
FT CONFLICT 265 265
SQ SEQUENCE 339 AA: 37363 MM; E105ED29518507EC CRC64;

Query Match 34.3%; Score 502.5; DB 1; Length 339;
Best local Similarity 39.2%; Pred. No. 5.3e-35;
Matches 111; Conservative 50; Mismatches 101; Indels 21; Gaps 6;

1 MENTENSVDSKSKLNLEPKTI--HGSSMSGSLSDSYKMDYPMGLCTIINKNFKHS 58
59 LANGYSSPSSSYKKNVAKMTDRHAE-----YNNRHRNRMALFNEHEHEVP 107
59 TGMTSRSGTDVDANRETFRNLTKEVYRNKNDLTREIEVELMDRVSKEDSKRSFQVL 118
108 T-LKSRAGTNVDENLRLVAKQDFEYTVYKDKRYKIDLTIEYASONSDDSCILVAI 166
119 LSHGEGCIIIFGNGPVDEKKTNEFFRDCRSLTGKPKLFIIACRGTEIDCGI-----E 173
167 LSHGEMGYIYAKDQYKLDINWISFFANHCPSLAGKPKLFIIQACGDRIDGVTMGRSQ 226
174 TDSGVDDMACHTIPEADFLVYSTAPGYSNRNSDGSWFIOSLCAMLKYADKLEFM 233
227 TETDGSWS-KYIPVHAFILAVSYVPGFSWRNRTGRWFMQSLCAELANLGRKIDIL 285
234 HILTVNRKRYATEFESEFSDA-TEHAKKOIPICVSMTKELYE 275
286 TLITFVQRYAVADFESCTEDTPRMHOKQIPICTITMLTRILRF 328

```
RESULT 12
ICE1_SPOFR
ID ICE1_SPOFR STANDARD: PRT: 299 AA.
AC P89116:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
```

OC Dityrria: Noctuoidea; Noctuidae; Amphipyridae; Spodoptera.
 OX NCBI_Taxid=7108;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97153084; PubMed=899805;
 RA Ahmed M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T.,
 RA Alnemri E.S.;
 RT "Spodoptera frugiperda caspase-1, a novel insect death protease that
 RT cleaves the nuclear immunophilin FKBP46, is the target of the
 RT baculovirus antiapoptotic protein p35.";
 RL J. Biol. Chem. 272:1421-1424(1997).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY). INHIBITED BY
 CC THE BACULOVIRUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35 AND
 CC NUCLEAR IMMUNOPHILIN FKBP46.
 CC -1- SUBUNIT: HETERODIMER OF A 19/18 kDa (P19/18) AND A 12 kDa (P12)
 CC SUBUNIT.
 CC -1- PTM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-stb.ch).
 CC -----
 CC EMBL: U81510; AAC47442.1; -
 CC DR HSSP: P42574; ICP3.
 CC DR MEROPS: C14.015; -
 CC DR InterPro: IPR002398; ICE.
 CC DR InterPro: IPR002138; ICE_P10.
 CC DR InterPro: IPR001309; ICE_P20.
 CC Pfam: PF00655; ICE_P10; 1.
 CC DR Pfam: PF00656; ICE_P20; 1.
 CC DR SMART: SM00115; CASC; 1.
 CC DR PROSITE: PS01122; CASPASE_CYS; 1.
 CC DR PROSITE: PS01121; CASPASE_HIS; 1.
 CC DR PROSITE: PS50207; CASPASE_P10; 1.
 CC DR PROSITE: PS50208; CASPASE_P20; 1.
 CC Hydrolyse: Thiol protease; Zymogen; Apoptosis.
 CC FT PROPEP 1 28
 CC FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.
 CC FT PROPEP 185 195 POTENTIAL.
 CC FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.
 CC FT ACT_SITE 136 136 BY SIMILARITY.
 CC FT ACT_SITE 178 178 BY SIMILARITY.
 CC FT SEQUENCE 299 AA; 33527 MW; 99FAFED09B04EEDC CRC64;
 SQ
 Query Match 32.1%; Score 470; DB 1; Length 299;
 Best Local Similarity 40.5%; Pred. No. 2,4e-32;
 Matches 100; Conservative 50; Mismatches 83; Indels 14; Gaps 5;

OY 37 YKNDYPEMGLCIINKNF--HKSTGMTSGTVDVAANLRETFRNKLYEVNRKNDLTRE 94
 Db 53 YNNHNRKGAALIEHNEHDH---SLKSTGTINVDSDNLSKVLKLTGEVTVFPPNKKSE 109
 OY 95 EIVELMRDYKSKEDHRSRVVCLSHGEGILFTGNGPVLDLKKITNFFRGDCRSITGK 154
 Db 110 EINKFTIOQTAEHMDADCLVALVTHGELGMLYAKDTYHKPNMLWYTFADRCPTLAG 169
 OY 155 PKLIITQACRGTELDGCI-----ETDSQVDDMACIKIPVPEADFLYATGAPGYISRRNS 209
 Db 170 PKLIITQACRGTELDGCI-----ETDSQVDDMACIKIPVPEADFLYATGAPGYISRRNS 226
 OY 210 KDSWFIQSLCALKOYADKLEFMHILTRVNRKVAATEFESFSD-ATFPAKDIPICTSM 268
 Db 227 TGSWFMQALCELRKAGTERDILITLTVYCKVALDFESNAPDSAMHQOKVPCITSM 286
 OY 269 LTRKELF 275
 Db 287 LTRLLVF 293

RESULT 13
 ID ICEL DROME
 AC 002002; 09WIN0; STANDARD; PRT: 323 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-1 precursor (EC 3.4.22.-).
 OS DCP-1 OR CG5370.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.
 RC TISSUE=Embryo;
 RX MEDLINE=97153052; PubMed=8999799;
 RA Song Z., McCall K., Steller H.;
 RT "DCP-1, a Drosophila cell death protease essential for development.";
 RL Science 275:536-540(1997).
 RN [2]
 RP ERRATUM.
 RA Song Z., McCall K., Steller H.;
 RL Science 277:167-167(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Baileon R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheele F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).
 CC PROPELYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). LOSS
 CC OF ZYGOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANOTIC

CC TUMORS.
 CC -1- SUBUNIT. HETERODIMER OF A 22 kDa (P22) AND A 13 kDa (P13) SUBUNIT.
 CC -1- DEVELOPMENTAL STAGE: PRESENT UNIFORMLY THROUGHOUT EMBRYOS OF
 CC STAGES 4 AND 10. IN STAGE 16 EMBRYOS, THE EXPRESSION BECOMES
 CC RESTRICTED TO THE CENTRAL NERVOUS SYSTEM, THE DEVELOPING GONADS,
 CC AND A PORTION OF THE GUT. IN STAGE 17 EMBRYOS, EXPRESSION IS
 CC MAINLY LOCALIZED IN CELLS ALONG THE MIDLINE OF THE CENTRAL NERVOUS
 CC SYSTEM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF001464; AAB58237.1; -;
 CC EMBL: AE003461; AAF47027.1; -;
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.016; -;
 CC FLYBASE: FBgn0010501; Dep-1.
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR002338; ICE_p10.
 CC InterPro: IPR001309; ICE_p20.
 CC Pfam: PF00655; ICE_p10; 1.
 CC Pfam: PF00656; ICE_p20; 1.
 CC PRINTS: PR00376; ILBCEZYME.
 CC SMART: SM00115; CASc; 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS50207; CASPASE_P10; 1.
 CC PROSITE: PS50208; CASPASE_P20; 1.
 CC Hydrolase: Thiol protease; Zymogen: Apoptosis.
 CC PROPEP 1 33 PROBABLE:
 CC CHAIN 34 202 CASPASE-1 SUBUNIT P22.
 CC PROPEP 203 215
 CC CHAIN 216 323 CASPASE-1 SUBUNIT P13.
 CC ACT_SITE 154 154 BY SIMILARITY.
 CC ACT_SITE 196 196 BY SIMILARITY.
 CC SEQUENCE 323 AA; 35926 MW; B5F0FF75EB8E2BD CRC64;
 CC
 CC Query Match 32.1%; Score 469; DB 1; Length 323;
 CC Best Local Similarity 39.7%; Pred. No. 3.3e-32;
 CC Matches 98; Conservative 46; Mismatches 95; Indels 8; Gaps 4;

ICB8_HUMAN STANDARD: PRT: 479 AA.
 AC 014790; 014791; 014792; 014794; 014795; 014796; 015780;
 AC 015806; 090081; 014676;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
 DE (MORTI-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
 DE like protease) (FADD-like ICE) (Flice) (Apoptotic cysteine protease)
 DE (Apoptotic protease Mch-5) (CASP4).
 GN CASP8 OR MCH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 OX 11
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Thymus, and B-cell.
 RX MEDLINE=96279826; PubMed=8681376;
 RA Boldo M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
 RT "Involvement of MACH, a novel MORTI/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death."; Cell
 RL Cell 85:803-815(1996).
 RN 12
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96279827; PubMed=8681377;
 RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Kramer P.H., Peter M.E., Dixit V.M.;
 RT "Flice, a novel FADD-homologous ICE/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex."; Cell
 RL Cell 85:817-827(1996).
 RN 13
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandez-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritsch L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemir E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN 14
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99132295; PubMed=9931493;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human CASP8 gene."; J
 RL Gene 226:225-232(1999).
 RN 15
 RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
 RX MEDLINE=97373543; PubMed=9228018;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemir T., Litwack G.,
 RA Armstrong R.C., Alnemir E.S.;
 RT "FLAME, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis."; J
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN 16
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemir T., Litwack G.,
 RA Alnemir E.S.;
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
 RT protease Mch5 is a Crma-inhibitable protease that activates multiple
 RT Ced-3/ICE-like cysteine proteases."; J
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 RN 17
 RP FUNCTION.
 RX MEDLINE=97160607; PubMed=9006941;
 RA Muzio M., Salvesen G.S., Dixit V.M.;
 RT "Flice induced apoptosis in a cell-free system. Cleavage of caspase
 RT zymogens."; J
 RL J. Biol. Chem. 272:2952-2956(1997).
 RN 18
 RP PROCESSING.
 RX MEDLINE=97327557; PubMed=9184224;

RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
 RA Kramer P.H., Peter M.E.: "FLICE is activated by association with the CD95 death-inducing
 RT signaling complex (DISC)."
 RT EMBO J. 16:2794-2804(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS):
 RX MEDLINE:99451259; PubMed:10508784;
 RA Blanchard H., Kodandapani L., Mittle P.R.E., Di Marco S., Krebs J.F.,
 RA Wu J.C., Tomaselli K.J., Grutter M.G.:
 RT "The three-dimensional structure of caspase-8: an initiator enzyme in
 RT apoptosis."
 RT Structure 7:1125-1133(1999).
 CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
 CC TNF-1 INDUCED CELL DEATH. BINDING TO THE ADAPTOR MOLECULE FADD
 CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED
 CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
 CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
 CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.
 CC CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY
 CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYSES THE SMALL-
 CC MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-1-AMC. LIKELY TARGET FOR
 CC THE COMPOX VIRUS CRMA DEATH INHIBITORY PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 10 kDa (P10) SUBUNIT.
 CC INTERACTS WITH CFLAR.
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS: 1-ALPHA (SHOWN HERE), 2-
 CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-
 CC BETA. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A
 CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD
 CC LEUCOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,
 CC TESTIS, AND SKELETAL MUSCLE.
 CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE
 CC DISC. WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE
 CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND
 CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X98172; CA66853.1; -
 DR EMBL: X98173; CA66854.1; -
 DR EMBL: X98174; CA66855.1; -
 DR EMBL: X98175; CA66856.1; -
 DR EMBL: X98176; CA66857.1; -
 DR EMBL: X98177; CA66858.1; -
 DR EMBL: X98178; CA66859.1; -
 DR EMBL: U58143; AAC50602.1; -
 DR EMBL: U60520; AAC50645.1; -
 DR EMBL: AF102146; AAD24962.1; -
 DR EMBL: AF102139; AAD24962.1; JOINED.
 DR EMBL: AF102140; AAD24962.1; JOINED.
 DR EMBL: AF102141; AAD24962.1; JOINED.
 DR EMBL: AF102142; AAD24962.1; JOINED.
 DR EMBL: AF102143; AAD24962.1; JOINED.
 DR EMBL: AF102144; AAD24962.1; JOINED.
 DR EMBL: AF102145; AAD24962.1; JOINED.
 DR EMBL: AF009620; AAB70913.1; -
 DR PDB: 1ODU; 10-JUL-00.
 DR MEROPS: C14.009; -
 DR Genem: HGNC:1509; CASP8.
 DR MIM: 601763; -

DR InterPro: IPR001875; DED.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR Pfam: PF01335; DED; 2.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS50168; DED; 2.
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;
 KW Repeat; 3D-structure.
 FT PROPEP 1 216
 FT CHAIN 217 374
 FT PROPEP 375 384
 FT CHAIN 385 479
 FT ACT_SITE 317 317
 FT ACT_SITE 360 360
 FT DOMAIN 2 80
 FT DOMAIN 100 177
 FT VASPLIC 102 102
 FT VASPLIC 184 198
 FT VASPLIC 184 220
 FT VASPLIC 184 267
 FT VASPLIC 199 235
 FT VASPLIC 221 479
 FT VASPLIC 236 479
 FT VASPLIC 269 276
 FT VASPLIC 277 479
 FT CONFLICT 285 285
 FT CONFLICT 294 294
 FT CONFLICT 331 331
 SO SEQUENCE 479 AA; 55391 MW; 7A5FEAA6B39B582F CRC64;
 Query March 28.8%; Score 421; DB 1; Length 479;
 Best Local Similarity 37.8%; Pred. No. 5.7e-28;
 Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;
 QY 24 SESMDSGISLDSNYKMDPEMGLCIITNNKFKHST-----GMTSRSGTDVDAANLRE 76
 DB 217 SESQ---TLDKVYQMKSKPRGYCLINNNHNPAAKAREKVPKLHSIRDRNGTHLDAGALT 272
 QY 77 TFRNLKIVYRNKNDITREIYELAMDVSKEDHSKSSFPYCVLLSHGEEIITGTNG-PVD 135
 DB 273 TFEELHFEIKPHDCTVBOIYEILKTYOLMDHSMNDCIFLHGDKIITGVTDGQEAP 332
 QY 136 LKLTNFRGDRGRSLTGKPKFLITQACRGTELDGI--ETDSG---VDDMAACKK--- 186
 DB 333 IYELTSQFTGLKCPSLAKPKVFYIOACGDNVYQKGIPEYVTSSEQPIYEMDLSQOTRY 392
 QY 187 IPVEADFLYASTAGYYSWRNSKSGSWFIOSLCAMLKQYADK-LEFMHILRVNKNVAT 245
 DB 393 IPDEADFLGMATVNNCGSYRNPAEGTWIISLQCSLRRCRGDDILITLLEVNVEVSN 452
 QY 246 EFESFSPDATHAKQIPIVSMLTKELYF 275
 DB 453 K-----DCKRMGKQMPQPTFLKKLVF 476
 RESULT 15
 ICE9_HUMAN STANDARD; PRT; 416 AA.
 ID ICE9_HUMAN AC P55211; O92852; O95348; Q9UBQ3;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCN-2001 (Rel. 40, last sequence update)
DT 15-OCN-2002 (Rel. 41, last annotation update)
DE Caspase-9 precursor (EC 3.4.22.-) (ICE-like apoptotic
DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
DE activating factor 3) (APAF-3).
GN CASP9 OR MCH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96279246; PubMed-8662294;
RA Duan H., Orsh K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
RA He W.-W., Dixit V.M.;
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
RT by the cytotoxic T cell protease granzyme B.";
RL J. Biol. Chem. 271:16720-16724(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PROCESSING.
RX TISSUE-T-cell;
RA MEDLINE-97059171; PubMed-8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trepant J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-99315341; PubMed-10384055;
RA Hadono S., Nasir J., Nichol K., Rasper D.M., Vallancourt J.P.,
RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
RT "Genomic organization of the human caspase-9 gene on chromosome
RT 1p36.1-p36.3.";
RL Mamm. Genome 10:757-760(1999).
RN [4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE-99168502; PubMed-10070954;
RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification of an endogenous dominant-negative short isoform of
RT caspase-9 that can regulate apoptosis.";
RL Cancer Res. 59:999-1002(1999).
RN [5]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX TISSUE-Stomach cancer;
RA Izawa M., Mori T., Ito H., Saiteji T.;
RT "Molecular cloning and sequencing of a cDNA predicting an alternative
RT form of pro-caspase-9 from human gastric cancer cell lines.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX Mino Y., Momoi T., Fujita E.;
RT "A novel splicing product of human caspase-9 lacking protease
RT activity.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE-99107856; PubMed-9890966;
RA Seol D.W., Billiar T.R.;
RT "A caspase-9 variant missing the catalytic site is an endogenous
RT inhibitor of apoptosis.";
RL J. Biol. Chem. 274:2072-2076(1999).
RN [8]
RP FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RP RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO APAF-
RP 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND
RP ACTIVATES CASPASE-3. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)
RP POLYMERASE (PARP).
CC - FUNCTION: THE SHORT ISOFORM LACKS ACTIVITY IS AN DOMINANT-NEGATIVE
CC INHIBITOR OF CASPASE-9.
CC - SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.

CC Caspase-9 and APAF1 bind to each other via their respective NH2-
CC terminal CED-3 homologous domains in the presence of cytochrome C
CC and ATP. Interacts with BIRC7
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG/9L/ALPHA FORM (SHOWN
CC HERE) AND A SHORT/9S/BETA FORM; ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC - TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHEST EXPRESSION IN THE
CC HEART, MODERATE EXPRESSION IN LIVER, SKELETAL MUSCLE, AND
CC PANCREAS. LOW LEVELS IN ALL OTHER TISSUES.
CC - PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
CC INVOLVED IN THESE PROCESSING EVENTS.
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U56390; AAC50640.1; -;
CC EMBL; U60521; AAC50776.1; -;
CC EMBL; AB019205; BAA82697.1; -;
CC EMBL; AB019197; BAA82697.1; JOINED.
CC EMBL; AB019198; BAA82697.1; JOINED.
CC EMBL; AB019199; BAA82697.1; JOINED.
CC EMBL; AB019200; BAA82697.1; JOINED.
CC EMBL; AB019201; BAA82697.1; JOINED.
CC EMBL; AB019202; BAA82697.1; JOINED.
CC EMBL; AB019203; BAA82697.1; JOINED.
CC EMBL; AB019204; BAA82697.1; JOINED.
CC EMBL; AF093130; AAD12248.1; -;
CC EMBL; AF093150; AAD12248.1; -;
CC EMBL; AB020979; BAA87905.1; -;
CC EMBL; AF110376; AAD13615.1; -;
CC HSP: P42574; 1PAU.
CC MEROPS; C14.010; -;
CC Genew; HGNC:1511; CASP9.
CC MIM; 602234; -;
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_P10.
CC InterPro; IPR001309; ICE_P20.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00655; ICE_P10; 1.
CC Pfam; PF00656; ICE_P20; 1.
CC PRINTS; PR00376; TL1BCENZME.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; zymogen; Apoptosis; Alternative splicing.
CC PROPEP 1 ?
CC CHAIN ? 315
CC PROPEP 316 330
CC CHAIN 331 416
CC DOMAIN 1 92
CC ACT_SITE 237 237
CC ACT_SITE 287 287
CC VARSPIC 140 289
CC CONFLICT 28 28
CC CONFLICT 32 32
CC CONFLICT 36 36
CC CONFLICT 96 96
CC CONFLICT 197 197
CC CONFLICT 221 221
CC SEQUENCE 416 AA; 46195 MM; 874B90F17FBD4CD CRC64;

